STIC Search Report
Biotech-Chem Library

STIC Database Tracking Number: 167126

TO: Sarvamangala Devi	**From:** Beverly Shears
Art Unit: 1645	**Location:** Biotech-Chem Library
Location: REM 3C18	REM 1A54
Serial Number: 10/054536	**Phone:** 571-272-2528
	beverly.shears@uspto.gov
Tuesday, June 21, 2005	

Search Notes

THIS PAGE BLANK (USPTO)

157126

Shears, Beverly

From: Devi, Sarvamangala
Sent: Friday, June 17, 2005 7:42 AM
To: Shears, Beverly
Subject: 10/054,536

Beverly:

In application 10/054,536, please perform a sequence search for SEQ ID NO: 2 in commercial and pending databases.

Thanx.

S. DEVI, Ph.D.
AU 1645
Rems - 3C18

BEST AVAILABLE COPY

Date completed: _____
Searcher: Beverly e 2528
Terminal time: _____
Elapsed time: _____
CPU time: _____
Total time: _____
Number of Searches: _____
Number of Databases: _____

Search Site

_____ STIC
_____ CM-1
_____ Pre-S

Type of Search

_____ N.A. Sequence
_____ A.A. Sequence
_____ Structure
_____ Bibliographic

Vendors

_____ IG
_____ STN
_____ Dialog
_____ APS
_____ Geninfo
_____ SDC
_____ DARC/Questel
_____ Other (CGN)

THIS PAGE BLANK (USPTO)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 19, 2005, 15:45:05 ; Search time 3604 Seconds
(without alignments)
10043.298 Million cell updates/sec

Title: US-10-054-536-2
Perfect score: 747
Sequence: 1 atgtccctgtttccatcact.....tctgtgagttccctatctga 747

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:*
1: gb_ba:*
2: gb_htg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vi:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	747	100.0	747	6	E27637	E27637 Recombinant
2	747	100.0	900	6	AR182149	AR182149 Sequence
3	747	100.0	1632	6	CQ875887	CQ875887 Sequence
4	747	100.0	1632	9	HOSA16576	Y16576 Homo sapien
5	747	100.0	1638	6	CQ875888	CQ875888 Sequence
6	747	100.0	1638	6	CQ875891	CQ875891 Sequence
7	747	100.0	1638	6	CQ875893	CQ875893 Sequence
8	747	100.0	1638	9	HOSA16577	Y16577 Homo sapien
9	747	100.0	1638	9	HOSA16580	Y16580 Homo sapien
10	747	100.0	1638	9	HOSA16581	Y16581 Homo sapien
11	747	100.0	3605	6	E27636	E27636 Recombinant
12	747	100.0	3605	6	AX411061	AX411061 Sequence
13	747	100.0	3605	9	HSMBPC	X15422 Human mRNA
14	745.4	99.8	960	9	BC069338	BC069338 Homo sapi
15	745.4	99.8	1632	6	CQ875889	CQ875889 Sequence
16	745.4	99.8	1632	9	HOSA16578	Y16578 Homo sapien
17	745.4	99.8	1638	6	CQ875890	CQ875890 Sequence
18	745.4	99.8	1638	6	CQ875892	CQ875892 Sequence
19	745.4	99.8	1638	9	HOSA16579	Y16579 Homo sapien
20	745.4	99.8	1638	9	HOSA16582	Y16582 Homo sapien
21	743.8	99.6	776	9	AF360991	AF360991 Homo sapi
22	635.8	85.1	1188	6	I09220	I09220 Sequence 1
23	599	80.2	678	6	CQ722821	CQ722821 Sequence
24	587.8	78.7	805	9	MACMBPC	L43911 Macaca mula
25	444.6	59.5	1409	4	D73408	D73408 Bos taurus
26	406.6	54.4	723	4	AF164576	AF164576 Sus scrof
27	395	52.9	1010	6	E37364	E37364 Swine serum
28	381.4	51.1	799	9	MACMBPA	L43912 Macaca mula
29	374.8	50.2	1116	10	S42294	S42294 mannose-bin
30	374	50.1	1254	9	HSMBP1D	X15957 H.sapiens M
31	374	50.1	3336	9	HSMBPCA3	AF080510 Homo sapi
32	373.2	50.0	1069	10	MUSRRFA	D11440 Mus musculu
33	373.2	50.0	1098	10	BC010760	BC010760 Mus muscu
34	372.4	49.9	374	9	AY707496S4	AY707499 Gorilla g
c 35	372.4	49.9	102532	9	AL731550	AL731550 Human DNA
36	370.8	49.6	374	9	AY707484S4	AY707487 Pan trogl
c 37	370.8	49.6	302859	2	AC044785	AC044785 Homo sapi
38	366.2	49.0	874	10	RNMBPR	X05023 Rat mRNA fo
39	364.6	48.8	1037	6	AX402034	AX402034 Sequence
40	364.6	48.8	1037	10	RATMABPC	M14103 Rat mannose
41	362.8	48.6	374	9	AY707480S4	AY707483 Pongo pyg
42	353.2	47.3	374	9	AY707504S4	AY707507 Hylobates
43	351.6	47.1	374	9	AY707500S4	AY707503 Hylobates
44	337.2	45.1	374	9	AY707516S4	AY707519 Presbytis
45	334	44.7	374	9	AY707476S4	AY707479 Papio pap

ALIGNMENTS

RESULT 1
E27637
LOCUS E27637 747 bp DNA linear PAT 18-JUN-2001
DEFINITION Recombinant human mannan binding protein and process for producing the same.
ACCESSION E27637
VERSION E27637.1 GI:13018239
KEYWORDS JP 1999206378-A/2.
SOURCE unidentified
ORGANISM unidentified
unclassified.
REFERENCE 1 (bases 1 to 747)
AUTHORS Nobutaka,W.
TITLE Recombinant human mannan binding protein and process for producing the same
JOURNAL Patent: JP 1999206378-A 2 03-AUG-1999;
FUSO YAKUHIN KOGYO KK
COMMENT OS Unidentified
PN JP 1999206378-A/2
PD 03-AUG-1999
PF 23-JAN-1998 JP 1998011864
PR
PI NOBUTAKA WAKAMIYA
PC C12N15/09,C07K14/47,C12P21/02//A61K38/00,(C12N15/09,C12R1:91),
PC (C12P21/02,C12R1:91),C12N15/00,A61K37/02,(C12N15/00,C12R1:91)
CC Strandedness: Double;
CC Topology: Linear;
FH Key Location/Qualifiers
FT source 1. .747
FT /organism='Unidentified'.
FEATURES Location/Qualifiers
source 1. .747
/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"
ORIGIN

Query Match 100.0%; Score 747; DB 6; Length 747;
Best Local Similarity 100.0%; Pred. No. 7.5e-209;
Matches 747; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGTCCCTGTTTCCATCACTCCCTCTCCTTCTCCTGAGTATGGTGGCAGCGTCTTACTCA 60

```
Db          1 ATGTCCCTGTTTCCATCACTCCCTCTCCTTCTCCTGAGTATGGTGGCAGCGTCTTACTCA 60
Qy         61 GAAACTGTGACCTGTGAGGATGCCCAAAAGACCTGCCCTGCAGTGATTGCCTGTAGCTCT 120
Db         61 GAAACTGTGACCTGTGAGGATGCCCAAAAGACCTGCCCTGCAGTGATTGCCTGTAGCTCT 120
Qy        121 CCAGGCATCAACGGCTTCCCAGGCAAAGATGGGCGTGATGGCACCAAGGGAGAAAAGGGG 180
Db        121 CCAGGCATCAACGGCTTCCCAGGCAAAGATGGGCGTGATGGCACCAAGGGAGAAAAGGGG 180
Qy        181 GAACCAGGCCAAGGGCTCAGAGGCTTACAGGGCCCCCCTGGAAAGTTGGGGCCTCCAGGA 240
Db        181 GAACCAGGCCAAGGGCTCAGAGGCTTACAGGGCCCCCCTGGAAAGTTGGGGCCTCCAGGA 240
Qy        241 AATCCAGGGCCTTCTGGGTCACCAGGACCAAAGGGCCAAAAAGGAGACCCTGGAAAAAGT 300
Db        241 AATCCAGGGCCTTCTGGGTCACCAGGACCAAAGGGCCAAAAAGGAGACCCTGGAAAAAGT 300
Qy        301 CCGGATGGTGATAGTAGCCTGGCTGCCTCAGAAAGAAAAGCTCTGCAAACAGAAATGGCA 360
Db        301 CCGGATGGTGATAGTAGCCTGGCTGCCTCAGAAAGAAAAGCTCTGCAAACAGAAATGGCA 360
Qy        361 CGTATCAAAAAGTGGCTGACCTTCTCTCTCTGGGCAAACAAGTTGGGAACAAGTTCTTCCTG 420
Db        361 CGTATCAAAAAGTGGCTGACCTTCTCTCTCTGGGCAAACAAGTTGGGAACAAGTTCTTCCTG 420
Qy        421 ACCAATGGTGAAATAATGACCTTTGAAAAAGTGAAGGCCTTGTGTGTCAAGTTCCAGGCC 480
Db        421 ACCAATGGTGAAATAATGACCTTTGAAAAAGTGAAGGCCTTGTGTGTCAAGTTCCAGGCC 480
Qy        481 TCTGTGGCCACCCCCAGGAATGCTGCAGAGAATGGAGCCATTCAGAATCTCATCAAGGAG 540
Db        481 TCTGTGGCCACCCCCAGGAATGCTGCAGAGAATGGAGCCATTCAGAATCTCATCAAGGAG 540
Qy        541 GAAGCCTTCCTGGGCATCACTGATGAGAAGACAGAAGGGCAGTTTGTGGATCTGACAGGA 600
Db        541 GAAGCCTTCCTGGGCATCACTGATGAGAAGACAGAAGGGCAGTTTGTGGATCTGACAGGA 600
Qy        601 AATAGACTGACCTACACAAACTGGAACGAGGGTGAACCCAACAATGCTGGTTCTGATGAA 660
Db        601 AATAGACTGACCTACACAAACTGGAACGAGGGTGAACCCAACAATGCTGGTTCTGATGAA 660
Qy        661 GATTGTGTATTGCTACTGAAAAATGGCCAGTGGAATGACGTCCCCTGCTCCACCTCCCAT 720
Db        661 GATTGTGTATTGCTACTGAAAAATGGCCAGTGGAATGACGTCCCCTGCTCCACCTCCCAT 720
Qy        721 CTGGCCGTCTGTGAGTTCCCTATCTGA 747
Db        721 CTGGCCGTCTGTGAGTTCCCTATCTGA 747
```

```
RESULT 2
AR182149
LOCUS       AR182149                900 bp    DNA     linear   PAT 20-APR-2002
DEFINITION  Sequence 1 from patent US 6337193.
ACCESSION   AR182149
VERSION     AR182149.1  GI:20225065
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 900)
  AUTHORS   Tully,R.E., Caltagirone,G.Thomas., Moyer,S.S. and Ronning,M.T.
  TITLE     Expression of manose-binding protein in methylotrophic yeast
  JOURNAL   Patent: US 6337193-A 1 08-JAN-2002;
FEATURES             Location/Qualifiers
     source          1. .900
                     /organism="unknown"
                     /mol_type="unassigned DNA"
ORIGIN

  Query Match             100.0%;  Score 747;  DB 6;  Length 900;
```

Best Local Similarity 100.0%; Pred. No. 7.7e-209;
Matches 747; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 ATGTCCCTGTTTCCATCACTCCCTCTCCTTCTCCTGAGTATGGTGGCAGCGTCTTACTCA 60
Db         66 ATGTCCCTGTTTCCATCACTCCCTCTCCTTCTCCTGAGTATGGTGGCAGCGTCTTACTCA 125
Qy         61 GAAACTGTGACCTGTGAGGATGCCCAAAAGACCTGCCCTGCAGTGATTGCCTGTAGCTCT 120
Db        126 GAAACTGTGACCTGTGAGGATGCCCAAAAGACCTGCCCTGCAGTGATTGCCTGTAGCTCT 185
Qy        121 CCAGGCATCAACGGCTTCCCAGGCAAAGATGGGCGTGATGGCACCAAGGGAGAAAAGGGG 180
Db        186 CCAGGCATCAACGGCTTCCCAGGCAAAGATGGGCGTGATGGCACCAAGGGAGAAAAGGGG 245
Qy        181 GAACCAGGCCAAGGGCTCAGAGGCTTACAGGGCCCCCCTGGAAAGTTGGGGCCTCCAGGA 240
Db        246 GAACCAGGCCAAGGGCTCAGAGGCTTACAGGGCCCCCCTGGAAAGTTGGGGCCTCCAGGA 305
Qy        241 AATCCAGGGCCTTCTGGGTCACCAGGACCAAAGGGCCAAAAAGGAGACCCTGGAAAAAGT 300
Db        306 AATCCAGGGCCTTCTGGGTCACCAGGACCAAAGGGCCAAAAAGGAGACCCTGGAAAAAGT 365
Qy        301 CCGGATGGTGATAGTAGCCTGGCTGCCTCAGAAAGAAAAGCTCTGCAAACAGAAATGGCA 360
Db        366 CCGGATGGTGATAGTAGCCTGGCTGCCTCAGAAAGAAAAGCTCTGCAAACAGAAATGGCA 425
Qy        361 CGTATCAAAAAGTGGCTGACCTTCTCTCTCTGGGCAAACAAGTTGGGAACAAGTTCTTCCTG 420
Db        426 CGTATCAAAAAGTGGCTGACCTTCTCTCTCTGGGCAAACAAGTTGGGAACAAGTTCTTCCTG 485
Qy        421 ACCAATGGTGAAATAATGACCTTTGAAAAAGTGAAGGCCTTGTGTGTCAAGTTCCAGGCC 480
Db        486 ACCAATGGTGAAATAATGACCTTTGAAAAAGTGAAGGCCTTGTGTGTCAAGTTCCAGGCC 545
Qy        481 TCTGTGGCCACCCCCAGGAATGCTGCAGAGAATGGAGCCATTCAGAATCTCATCAAGGAG 540
Db        546 TCTGTGGCCACCCCCAGGAATGCTGCAGAGAATGGAGCCATTCAGAATCTCATCAAGGAG 605
Qy        541 GAAGCCTTCCTGGGCATCACTGATGAGAAGACAGAAGGGCAGTTTGTGGATCTGACAGGA 600
Db        606 GAAGCCTTCCTGGGCATCACTGATGAGAAGACAGAAGGGCAGTTTGTGGATCTGACAGGA 665
Qy        601 AATAGACTGACCTACACAAACTGGAACGAGGGTGAACCCAACAATGCTGGTTCTGATGAA 660
Db        666 AATAGACTGACCTACACAAACTGGAACGAGGGTGAACCCAACAATGCTGGTTCTGATGAA 725
Qy        661 GATTGTGTATTGCTACTGAAAAATGGCCAGTGGAATGACGTCCCCTGCTCCACCTCCCAT 720
Db        726 GATTGTGTATTGCTACTGAAAAATGGCCAGTGGAATGACGTCCCCTGCTCCACCTCCCAT 785
Qy        721 CTGGCCGTCTGTGAGTTCCCTATCTGA 747
Db        786 CTGGCCGTCTGTGAGTTCCCTATCTGA 812
```

```
RESULT 3
CQ875887
LOCUS       CQ875887                1632 bp    DNA     linear   PAT 04-OCT-2004
DEFINITION  Sequence 20 from Patent WO2004065626.
ACCESSION   CQ875887
VERSION     CQ875887.1  GI:53789630
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Garred,P., Madsen,H.O. and str M,J.
  TITLE     A method of sepsis prognosis
  JOURNAL   Patent: WO 2004065626-A 20 05-AUG-2004;
            Rigshospitalet (DK); Kobenhavns Amt (DK)
FEATURES             Location/Qualifiers
```

```
     source          1. .1632
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
ORIGIN

  Query Match             100.0%;  Score 747;  DB 6;  Length 1632;
  Best Local Similarity   100.0%;  Pred. No. 8.2e-209;
  Matches  747;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATGTCCCTGTTTCCATCACTCCCTCTCCTTCTCCTGAGTATGGTGGCAGCGTCTTACTCA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        886 ATGTCCCTGTTTCCATCACTCCCTCTCCTTCTCCTGAGTATGGTGGCAGCGTCTTACTCA 945

Qy         61 GAAACTGTGACCTGTGAGGATGCCCAAAAGACCTGCCCTGCAGTGATTGCCTGTAGCTCT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        946 GAAACTGTGACCTGTGAGGATGCCCAAAAGACCTGCCCTGCAGTGATTGCCTGTAGCTCT 1005

Qy        121 CCAGGCATCAACGGCTTCCCAGGCAAAGATGGGCGTGATGGCACCAAGGGAGAAAAGGGG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1006 CCAGGCATCAACGGCTTCCCAGGCAAAGATGGGCGTGATGGCACCAAGGGAGAAAAGGGG 1065

Qy        181 GAACCAGGCCAAGGGCTCAGAGGCTTACAGGGCCCCCCTGGAAAGTTGGGGCCTCCAGGA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1066 GAACCAGGCCAAGGGCTCAGAGGCTTACAGGGCCCCCCTGGAAAGTTGGGGCCTCCAGGA 1125

Qy        241 AATCCAGGGCCTTCTGGGTCACCAGGACCAAAGGGCCAAAAAGGAGACCCTGGAAAAAGT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1126 AATCCAGGGCCTTCTGGGTCACCAGGACCAAAGGGCCAAAAAGGAGACCCTGGAAAAAGT 1185

Qy        301 CCGGATGGTGATAGTAGCCTGGCTGCCTCAGAAAGAAAAGCTCTGCAAACAGAAATGGCA 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1186 CCGGATGGTGATAGTAGCCTGGCTGCCTCAGAAAGAAAAGCTCTGCAAACAGAAATGGCA 1245

Qy        361 CGTATCAAAAAGTGGCTGACCTTCTCTCTGGGCAAACAAGTTGGGAACAAGTTCTTCCTG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1246 CGTATCAAAAAGTGGCTGACCTTCTCTCTGGGCAAACAAGTTGGGAACAAGTTCTTCCTG 1305

Qy        421 ACCAATGGTGAAATAATGACCTTTGAAAAAGTGAAGGCCTTGTGTGTCAAGTTCCAGGCC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1306 ACCAATGGTGAAATAATGACCTTTGAAAAAGTGAAGGCCTTGTGTGTCAAGTTCCAGGCC 1365

Qy        481 TCTGTGGCCACCCCCAGGAATGCTGCAGAGAATGGAGCCATTCAGAATCTCATCAAGGAG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1366 TCTGTGGCCACCCCCAGGAATGCTGCAGAGAATGGAGCCATTCAGAATCTCATCAAGGAG 1425

Qy        541 GAAGCCTTCCTGGGCATCACTGATGAGAAGACAGAAGGGCAGTTTGTGGATCTGACAGGA 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1426 GAAGCCTTCCTGGGCATCACTGATGAGAAGACAGAAGGGCAGTTTGTGGATCTGACAGGA 1485

Qy        601 AATAGACTGACCTACACAAACTGGAACGAGGGTGAACCCAACAATGCTGGTTCTGATGAA 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1486 AATAGACTGACCTACACAAACTGGAACGAGGGTGAACCCAACAATGCTGGTTCTGATGAA 1545

Qy        661 GATTGTGTATTGCTACTGAAAAATGGCCAGTGGAATGACGTCCCCTGCTCCACCTCCCAT 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1546 GATTGTGTATTGCTACTGAAAAATGGCCAGTGGAATGACGTCCCCTGCTCCACCTCCCAT 1605

Qy        721 CTGGCCGTCTGTGAGTTCCCTATCTGA 747
              ||||||||||||||||||||||||||
Db       1606 CTGGCCGTCTGTGAGTTCCCTATCTGA 1632


RESULT 4
HOSA16576
LOCUS       HOSA16576               1632 bp    DNA     linear   PRI 17-SEP-1999
DEFINITION  Homo sapiens gene encoding mannan/mannose-binding protein, variant
            LYQA.
ACCESSION   Y16576
VERSION     Y16576.1  GI:5911789
KEYWORDS    mannose-binding lectin; mbl gene.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Madsen,H.O., Satz,M.L., Hogh,B., Svejgaard,A. and Garred,P.
  TITLE     Different molecular events result in low protein levels of
            mannan-binding lectin in populations from southeast Africa and
            South America
  JOURNAL   J. Immunol. 161 (6), 3169-3175 (1998)
  MEDLINE   98414317
   PUBMED   9743385
REFERENCE   2  (bases 1 to 1632)
  AUTHORS   Madsen,H.O.
  TITLE     Direct Submission
  JOURNAL   Submitted (16-FEB-1998) H.O. Madsen, Department of Clinical
            Immunology, Section 7631, National University Hospital, Tagensvej
            20, DK-2200 Copenhagen, DENMARK
COMMENT     Related sequences  X15954, X15955, X15956, X15422.
FEATURES             Location/Qualifiers
     source          1. .1632
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
                     /chromosome="10"
                     /map="10q11.2-q21"
                     /note="MBL haplotype LYQA"
     variation       273
                     /note="polymorphism in different MBL haplotypes"
     variation       396
                     /note="polymorphism in different MBL haplotypes"
     variation       474
                     /note="polymorphism in different MBL haplotypes"
     variation       487
                     /note="polymorphism in different MBL haplotypes"
     variation       596
                     /note="polymorphism in different MBL haplotypes"
     variation       596
                     /note="polymorphism in different MBL haplotypes"
     gene            739. .1632
                     /gene="MBL"
     CAAT_signal     739. .744
                     /gene="MBL"
     variation       747
                     /gene="MBL"
                     /note="polymorphism in different MBL haplotypes"
     TATA_signal     780. .785
                     /gene="MBL"
     mRNA            817. .>1632
                     /gene="MBL"
                     /product="mannose-binding lectin"
     variation       820
                     /gene="MBL"
                     /note="polymorphism in different MBL haplotypes"
     CDS             886. .1632
                     /gene="MBL"
                     /codon_start=1
                     /product="mannose-binding lectin"
                     /protein_id="CAB56044.1"
                     /db_xref="GI:5911790"
                     /db_xref="GOA:P11226"
                     /db_xref="UniProt/Swiss-Prot:P11226"
                     /translation="MSLFPSLPLLLLSMVAASYSETVTCEDAQKTCPAVIACSSPGIN
                     GFPGKDGRDGTKGEKGEPGQGLRGLQGPPGKLGPPGNPGPSGSPGPKGQKGDPGKSPD
                     GDSSLAASERKALQTEMARIKKWLTFSLGKQVGNKFFLTNGEIMTFEKVKALCVKFQA
                     SVATPRNAAENGAIQNLIKEEAFLGITDEKTEGQFVDLTGNRLTYTNWNEGEPNNAGS
                     DEDCVLLLKNGQWNDVPCSTSHLAVCEFPI"
     sig_peptide     886. .945
                     /gene="MBL"
     variation       1039
                     /gene="MBL"
                     /note="polymorphism in different MBL haplotypes"
     variation       1046
                     /gene="MBL"
                     /note="polymorphism in different MBL haplotypes"
     variation       1055
                     /gene="MBL"
```

/note="polymorphism in different MBL haplotypes"

ORIGIN

Query Match 100.0%; Score 747; DB 9; Length 1632;
Best Local Similarity 100.0%; Pred. No. 8.2e-209;
Matches 747; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 ATGTCCCTGTTTCCATCACTCCCTCTCCTTCTCCTGAGTATGGTGGCAGCGTCTTACTCA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        886 ATGTCCCTGTTTCCATCACTCCCTCTCCTTCTCCTGAGTATGGTGGCAGCGTCTTACTCA 945

Qy         61 GAAACTGTGACCTGTGAGGATGCCCAAAAGACCTGCCCTGCAGTGATTGCCTGTAGCTCT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        946 GAAACTGTGACCTGTGAGGATGCCCAAAAGACCTGCCCTGCAGTGATTGCCTGTAGCTCT 1005

Qy        121 CCAGGCATCAACGGCTTCCCAGGCAAAGATGGGCGTGATGGCACCAAGGGAGAAAAGGGG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1006 CCAGGCATCAACGGCTTCCCAGGCAAAGATGGGCGTGATGGCACCAAGGGAGAAAAGGGG 1065

Qy        181 GAACCAGGCCAAGGGCTCAGAGGCTTACAGGGCCCCCCTGGAAAGTTGGGGCCTCCAGGA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1066 GAACCAGGCCAAGGGCTCAGAGGCTTACAGGGCCCCCCTGGAAAGTTGGGGCCTCCAGGA 1125

Qy        241 AATCCAGGGCCTTCTGGGTCACCAGGACCAAAGGGCCAAAAAGGAGACCCTGGAAAAAGT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1126 AATCCAGGGCCTTCTGGGTCACCAGGACCAAAGGGCCAAAAAGGAGACCCTGGAAAAAGT 1185

Qy        301 CCGGATGGTGATAGTAGCCTGGCTGCCTCAGAAAGAAAAGCTCTGCAAACAGAAATGGCA 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1186 CCGGATGGTGATAGTAGCCTGGCTGCCTCAGAAAGAAAAGCTCTGCAAACAGAAATGGCA 1245

Qy        361 CGTATCAAAAAGTGGCTGACCTTCTCTCTGGGCAAACAAGTTGGGAACAAGTTCTTCCTG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1246 CGTATCAAAAAGTGGCTGACCTTCTCTCTGGGCAAACAAGTTGGGAACAAGTTCTTCCTG 1305

Qy        421 ACCAATGGTGAAATAATGACCTTTGAAAAAGTGAAGGCCTTGTGTGTCAAGTTCCAGGCC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1306 ACCAATGGTGAAATAATGACCTTTGAAAAAGTGAAGGCCTTGTGTGTCAAGTTCCAGGCC 1365

Qy        481 TCTGTGGCCACCCCCAGGAATGCTGCAGAGAATGGAGCCATTCAGAATCTCATCAAGGAG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1366 TCTGTGGCCACCCCCAGGAATGCTGCAGAGAATGGAGCCATTCAGAATCTCATCAAGGAG 1425

Qy        541 GAAGCCTTCCTGGGCATCACTGATGAGAAGACAGAAGGGCAGTTTGTGGATCTGACAGGA 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1426 GAAGCCTTCCTGGGCATCACTGATGAGAAGACAGAAGGGCAGTTTGTGGATCTGACAGGA 1485

Qy        601 AATAGACTGACCTACACAAACTGGAACGAGGGTGAACCCAACAATGCTGGTTCTGATGAA 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1486 AATAGACTGACCTACACAAACTGGAACGAGGGTGAACCCAACAATGCTGGTTCTGATGAA 1545

Qy        661 GATTGTGTATTGCTACTGAAAAATGGCCAGTGGAATGACGTCCCCTGCTCCACCTCCCAT 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1546 GATTGTGTATTGCTACTGAAAAATGGCCAGTGGAATGACGTCCCCTGCTCCACCTCCCAT 1605

Qy        721 CTGGCCGTCTGTGAGTTCCCTATCTGA 747
              |||||||||||||||||||||||||||
Db       1606 CTGGCCGTCTGTGAGTTCCCTATCTGA 1632
```

RESULT 5
CQ875888
LOCUS CQ875888 1638 bp DNA linear PAT 04-OCT-2004
DEFINITION Sequence 21 from Patent WO2004065626.
ACCESSION CQ875888
VERSION CQ875888.1 GI:53789631
KEYWORDS .
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Garred,P., Madsen,H.O. and str M,J.
TITLE A method of sepsis prognosis
JOURNAL Patent: WO 2004065626-A 21 05-AUG-2004;
Rigshospitalet (DK); Kobenhavns Amt (DK)
FEATURES Location/Qualifiers
source 1. .1638
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN

Query Match 100.0%; Score 747; DB 6; Length 1638;
Best Local Similarity 100.0%; Pred. No. 8.2e-209;
Matches 747; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 ATGTCCCTGTTTCCATCACTCCCTCTCCTTCTCCTGAGTATGGTGGCAGCGTCTTACTCA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        892 ATGTCCCTGTTTCCATCACTCCCTCTCCTTCTCCTGAGTATGGTGGCAGCGTCTTACTCA 951

Qy         61 GAAACTGTGACCTGTGAGGATGCCCAAAAGACCTGCCCTGCAGTGATTGCCTGTAGCTCT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        952 GAAACTGTGACCTGTGAGGATGCCCAAAAGACCTGCCCTGCAGTGATTGCCTGTAGCTCT 1011

Qy        121 CCAGGCATCAACGGCTTCCCAGGCAAAGATGGGCGTGATGGCACCAAGGGAGAAAAGGGG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1012 CCAGGCATCAACGGCTTCCCAGGCAAAGATGGGCGTGATGGCACCAAGGGAGAAAAGGGG 1071

Qy        181 GAACCAGGCCAAGGGCTCAGAGGCTTACAGGGCCCCCCTGGAAAGTTGGGGCCTCCAGGA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1072 GAACCAGGCCAAGGGCTCAGAGGCTTACAGGGCCCCCCTGGAAAGTTGGGGCCTCCAGGA 1131

Qy        241 AATCCAGGGCCTTCTGGGTCACCAGGACCAAAGGGCCAAAAAGGAGACCCTGGAAAAAGT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1132 AATCCAGGGCCTTCTGGGTCACCAGGACCAAAGGGCCAAAAAGGAGACCCTGGAAAAAGT 1191

Qy        301 CCGGATGGTGATAGTAGCCTGGCTGCCTCAGAAAGAAAAGCTCTGCAAACAGAAATGGCA 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1192 CCGGATGGTGATAGTAGCCTGGCTGCCTCAGAAAGAAAAGCTCTGCAAACAGAAATGGCA 1251

Qy        361 CGTATCAAAAAGTGGCTGACCTTCTCTCTGGGCAAACAAGTTGGGAACAAGTTCTTCCTG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1252 CGTATCAAAAAGTGGCTGACCTTCTCTCTGGGCAAACAAGTTGGGAACAAGTTCTTCCTG 1311

Qy        421 ACCAATGGTGAAATAATGACCTTTGAAAAAGTGAAGGCCTTGTGTGTCAAGTTCCAGGCC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1312 ACCAATGGTGAAATAATGACCTTTGAAAAAGTGAAGGCCTTGTGTGTCAAGTTCCAGGCC 1371

Qy        481 TCTGTGGCCACCCCCAGGAATGCTGCAGAGAATGGAGCCATTCAGAATCTCATCAAGGAG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1372 TCTGTGGCCACCCCCAGGAATGCTGCAGAGAATGGAGCCATTCAGAATCTCATCAAGGAG 1431

Qy        541 GAAGCCTTCCTGGGCATCACTGATGAGAAGACAGAAGGGCAGTTTGTGGATCTGACAGGA 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1432 GAAGCCTTCCTGGGCATCACTGATGAGAAGACAGAAGGGCAGTTTGTGGATCTGACAGGA 1491

Qy        601 AATAGACTGACCTACACAAACTGGAACGAGGGTGAACCCAACAATGCTGGTTCTGATGAA 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1492 AATAGACTGACCTACACAAACTGGAACGAGGGTGAACCCAACAATGCTGGTTCTGATGAA 1551

Qy        661 GATTGTGTATTGCTACTGAAAAATGGCCAGTGGAATGACGTCCCCTGCTCCACCTCCCAT 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1552 GATTGTGTATTGCTACTGAAAAATGGCCAGTGGAATGACGTCCCCTGCTCCACCTCCCAT 1611

Qy        721 CTGGCCGTCTGTGAGTTCCCTATCTGA 747
              |||||||||||||||||||||||||||
Db       1612 CTGGCCGTCTGTGAGTTCCCTATCTGA 1638
```

RESULT 6
CQ875891
LOCUS CQ875891 1638 bp DNA linear PAT 04-OCT-2004
DEFINITION Sequence 24 from Patent WO2004065626.
ACCESSION CQ875891
VERSION CQ875891.1 GI:53789634

```
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Garred,P., Madsen,H.O. and str M,J.
  TITLE     A method of sepsis prognosis
  JOURNAL   Patent: WO 2004065626-A 24 05-AUG-2004;
            Rigshospitalet (DK); Kobenhavns Amt (DK)
FEATURES             Location/Qualifiers
     source          1. .1638
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
ORIGIN

  Query Match             100.0%;  Score 747;  DB 6;  Length 1638;
  Best Local Similarity   100.0%;  Pred. No. 8.2e-209;
  Matches  747;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATGTCCCTGTTTCCATCACTCCCTCTCCTTCTCCTGAGTATGGTGGCAGCGTCTTACTCA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        892 ATGTCCCTGTTTCCATCACTCCCTCTCCTTCTCCTGAGTATGGTGGCAGCGTCTTACTCA 951

Qy         61 GAAACTGTGACCTGTGAGGATGCCCAAAAGACCTGCCCTGCAGTGATTGCCTGTAGCTCT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        952 GAAACTGTGACCTGTGAGGATGCCCAAAAGACCTGCCCTGCAGTGATTGCCTGTAGCTCT 1011

Qy        121 CCAGGCATCAACGGCTTCCCAGGCAAAGATGGGCGTGATGGCACCAAGGGAGAAAAGGGG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1012 CCAGGCATCAACGGCTTCCCAGGCAAAGATGGGCGTGATGGCACCAAGGGAGAAAAGGGG 1071

Qy        181 GAACCAGGCCAAGGGCTCAGAGGCTTACAGGGCCCCCCTGGAAAGTTGGGGCCTCCAGGA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1072 GAACCAGGCCAAGGGCTCAGAGGCTTACAGGGCCCCCCTGGAAAGTTGGGGCCTCCAGGA 1131

Qy        241 AATCCAGGGCCTTCTGGGTCACCAGGACCAAAGGGCCAAAAAGGAGACCCTGGAAAAAGT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1132 AATCCAGGGCCTTCTGGGTCACCAGGACCAAAGGGCCAAAAAGGAGACCCTGGAAAAAGT 1191

Qy        301 CCGGATGGTGATAGTAGCCTGGCTGCCTCAGAAAGAAAAGCTCTGCAAACAGAAATGGCA 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1192 CCGGATGGTGATAGTAGCCTGGCTGCCTCAGAAAGAAAAGCTCTGCAAACAGAAATGGCA 1251

Qy        361 CGTATCAAAAAGTGGCTGACCTTCTCTCTGGGCAAACAAGTTGGGAACAAGTTCTTCCTG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1252 CGTATCAAAAAGTGGCTGACCTTCTCTCTGGGCAAACAAGTTGGGAACAAGTTCTTCCTG 1311

Qy        421 ACCAATGGTGAAATAATGACCTTTGAAAAAGTGAAGGCCTTGTGTGTCAAGTTCCAGGCC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1312 ACCAATGGTGAAATAATGACCTTTGAAAAAGTGAAGGCCTTGTGTGTCAAGTTCCAGGCC 1371

Qy        481 TCTGTGGCCACCCCCAGGAATGCTGCAGAGAATGGAGCCATTCAGAATCTCATCAAGGAG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1372 TCTGTGGCCACCCCCAGGAATGCTGCAGAGAATGGAGCCATTCAGAATCTCATCAAGGAG 1431

Qy        541 GAAGCCTTCCTGGGCATCACTGATGAGAAGACAGAAGGGCAGTTTGTGGATCTGACAGGA 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1432 GAAGCCTTCCTGGGCATCACTGATGAGAAGACAGAAGGGCAGTTTGTGGATCTGACAGGA 1491

Qy        601 AATAGACTGACCTACACAAACTGGAACGAGGGTGAACCCAACAATGCTGGTTCTGATGAA 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1492 AATAGACTGACCTACACAAACTGGAACGAGGGTGAACCCAACAATGCTGGTTCTGATGAA 1551

Qy        661 GATTGTGTATTGCTACTGAAAAATGGCCAGTGGAATGACGTCCCCTGCTCCACCTCCCAT 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1552 GATTGTGTATTGCTACTGAAAAATGGCCAGTGGAATGACGTCCCCTGCTCCACCTCCCAT 1611

Qy        721 CTGGCCGTCTGTGAGTTCCCTATCTGA 747
              ||||||||||||||||||||||||||
Db       1612 CTGGCCGTCTGTGAGTTCCCTATCTGA 1638
```

```
RESULT 7
CQ875893
LOCUS       CQ875893                1638 bp    DNA     linear   PAT 04-OCT-2004
DEFINITION  Sequence 26 from Patent WO2004065626.
ACCESSION   CQ875893
VERSION     CQ875893.1  GI:53789636
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Garred,P., Madsen,H.O. and str M,J.
  TITLE     A method of sepsis prognosis
  JOURNAL   Patent: WO 2004065626-A 26 05-AUG-2004;
            Rigshospitalet (DK); Kobenhavns Amt (DK)
FEATURES             Location/Qualifiers
     source          1. .1638
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
ORIGIN

  Query Match             100.0%;  Score 747;  DB 6;  Length 1638;
  Best Local Similarity   100.0%;  Pred. No. 8.2e-209;
  Matches  747;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATGTCCCTGTTTCCATCACTCCCTCTCCTTCTCCTGAGTATGGTGGCAGCGTCTTACTCA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        892 ATGTCCCTGTTTCCATCACTCCCTCTCCTTCTCCTGAGTATGGTGGCAGCGTCTTACTCA 951

Qy         61 GAAACTGTGACCTGTGAGGATGCCCAAAAGACCTGCCCTGCAGTGATTGCCTGTAGCTCT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        952 GAAACTGTGACCTGTGAGGATGCCCAAAAGACCTGCCCTGCAGTGATTGCCTGTAGCTCT 1011

Qy        121 CCAGGCATCAACGGCTTCCCAGGCAAAGATGGGCGTGATGGCACCAAGGGAGAAAAGGGG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1012 CCAGGCATCAACGGCTTCCCAGGCAAAGATGGGCGTGATGGCACCAAGGGAGAAAAGGGG 1071

Qy        181 GAACCAGGCCAAGGGCTCAGAGGCTTACAGGGCCCCCCTGGAAAGTTGGGGCCTCCAGGA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1072 GAACCAGGCCAAGGGCTCAGAGGCTTACAGGGCCCCCCTGGAAAGTTGGGGCCTCCAGGA 1131

Qy        241 AATCCAGGGCCTTCTGGGTCACCAGGACCAAAGGGCCAAAAAGGAGACCCTGGAAAAAGT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1132 AATCCAGGGCCTTCTGGGTCACCAGGACCAAAGGGCCAAAAAGGAGACCCTGGAAAAAGT 1191

Qy        301 CCGGATGGTGATAGTAGCCTGGCTGCCTCAGAAAGAAAAGCTCTGCAAACAGAAATGGCA 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1192 CCGGATGGTGATAGTAGCCTGGCTGCCTCAGAAAGAAAAGCTCTGCAAACAGAAATGGCA 1251

Qy        361 CGTATCAAAAAGTGGCTGACCTTCTCTCTGGGCAAACAAGTTGGGAACAAGTTCTTCCTG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1252 CGTATCAAAAAGTGGCTGACCTTCTCTCTGGGCAAACAAGTTGGGAACAAGTTCTTCCTG 1311

Qy        421 ACCAATGGTGAAATAATGACCTTTGAAAAAGTGAAGGCCTTGTGTGTCAAGTTCCAGGCC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1312 ACCAATGGTGAAATAATGACCTTTGAAAAAGTGAAGGCCTTGTGTGTCAAGTTCCAGGCC 1371

Qy        481 TCTGTGGCCACCCCCAGGAATGCTGCAGAGAATGGAGCCATTCAGAATCTCATCAAGGAG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1372 TCTGTGGCCACCCCCAGGAATGCTGCAGAGAATGGAGCCATTCAGAATCTCATCAAGGAG 1431

Qy        541 GAAGCCTTCCTGGGCATCACTGATGAGAAGACAGAAGGGCAGTTTGTGGATCTGACAGGA 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1432 GAAGCCTTCCTGGGCATCACTGATGAGAAGACAGAAGGGCAGTTTGTGGATCTGACAGGA 1491

Qy        601 AATAGACTGACCTACACAAACTGGAACGAGGGTGAACCCAACAATGCTGGTTCTGATGAA 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1492 AATAGACTGACCTACACAAACTGGAACGAGGGTGAACCCAACAATGCTGGTTCTGATGAA 1551

Qy        661 GATTGTGTATTGCTACTGAAAAATGGCCAGTGGAATGACGTCCCCTGCTCCACCTCCCAT 720
```

```
                    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1552 GATTGTGTATTGCTACTGAAAAATGGCCAGTGGAATGACGTCCCCTGCTCCACCTCCCAT 1611

Qy        721 CTGGCCGTCTGTGAGTTCCCTATCTGA 747
              ||||||||||||||||||||||||||||
Db       1612 CTGGCCGTCTGTGAGTTCCCTATCTGA 1638


RESULT 8
HOSA16577
LOCUS       HOSA16577               1638 bp    DNA     linear   PRI 17-SEP-1999
DEFINITION  Homo sapiens gene encoding mannan/mannose-binding protein, variant
            LYPA.
ACCESSION   Y16577
VERSION     Y16577.1  GI:5911791
KEYWORDS    mannose-binding lectin; mbl gene.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Madsen,H.O., Satz,M.L., Hogh,B., Svejgaard,A. and Garred,P.
  TITLE     Different molecular events result in low protein levels of
            mannan-binding lectin in populations from southeast Africa and
            South America
  JOURNAL   J. Immunol. 161 (6), 3169-3175 (1998)
  MEDLINE   98414317
   PUBMED   9743385
REFERENCE   2  (bases 1 to 1638)
  AUTHORS   Madsen,H.O.
  TITLE     Direct Submission
  JOURNAL   Submitted (16-FEB-1998) H.O. Madsen, Department of Clinical
            Immunology, Section 7631, National University Hospital, Tagensvej
            20, DK-2200 Copenhagen, DENMARK
COMMENT     Related sequences  X15954, X15955, X15956, X15422.
FEATURES             Location/Qualifiers
     source          1. .1638
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
                     /chromosome="10"
                     /map="10q11.2-q21"
                     /note="MBL haplotype LYPA"
     variation       273
                     /note="polymorphism in different MBL haplotypes"
     variation       396
                     /note="polymorphism in different MBL haplotypes"
     variation       474
                     /note="polymorphism in different MBL haplotypes"
     variation       487
                     /note="polymorphism in different MBL haplotypes"
     variation       495. .500
                     /note="polymorphism in different MBL haplotypes"
     gene            745. .1638
                     /gene="MBL"
     CAAT_signal     745. .750
                     /gene="MBL"
     variation       753
                     /gene="MBL"
                     /note="polymorphism in different MBL haplotypes"
     TATA_signal     786. .791
                     /gene="MBL"
     mRNA            823. .>1638
                     /gene="MBL"
                     /product="mannose-binding lectin"
     variation       826
                     /gene="MBL"
                     /note="polymorphism in different MBL haplotypes"
     CDS             892. .1638
                     /gene="MBL"
                     /codon_start=1
                     /product="mannose-binding lectin"
                     /protein_id="CAB56120.1"
                     /db_xref="GI:5911792"
                     /db_xref="GOA:P11226"
                     /db_xref="UniProt/Swiss-Prot:P11226"
                     /translation="MSLFPSLPLLLLSMVAASYSETVTCEDAQKTCPAVIACSSPGIN
                     GFPGKDGRDGTKGEKGEPGQGLRGLQGPPGKLGPPGNPGPSGSPGPKGQKGDPGKSPD
                     GDSSLAASERKALQTEMARIKKWLTFSLGKQVGNKFFLTNGEIMTFEKVKALCVKFQA
                     SVATPRNAAENGAIQNLIKEEAFLGITDEKTEGQFVDLTGNRLTYTNWNEGEPNNAGS
                     DEDCVLLLKNGQWNDVPCSTSHLAVCEFPI"
     sig_peptide     892. .951
                     /gene="MBL"
     variation       1045
                     /gene="MBL"
                     /note="polymorphism in different MBL haplotypes"
     variation       1052
                     /gene="MBL"
                     /note="polymorphism in different MBL haplotypes"
     variation       1061
                     /gene="MBL"
                     /note="polymorphism in different MBL haplotypes"
ORIGIN

  Query Match             100.0%;  Score 747;  DB 9;  Length 1638;
  Best Local Similarity   100.0%;  Pred. No. 8.2e-209;
  Matches  747;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATGTCCCTGTTTCCATCACTCCCTCTCCTTCTCCTGAGTATGGTGGCAGCGTCTTACTCA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        892 ATGTCCCTGTTTCCATCACTCCCTCTCCTTCTCCTGAGTATGGTGGCAGCGTCTTACTCA 951

Qy         61 GAAACTGTGACCTGTGAGGATGCCCAAAAGACCTGCCCTGCAGTGATTGCCTGTAGCTCT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        952 GAAACTGTGACCTGTGAGGATGCCCAAAAGACCTGCCCTGCAGTGATTGCCTGTAGCTCT 1011

Qy        121 CCAGGCATCAACGGCTTCCCAGGCAAAGATGGGCGTGATGGCACCAAGGGAGAAAAGGGG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1012 CCAGGCATCAACGGCTTCCCAGGCAAAGATGGGCGTGATGGCACCAAGGGAGAAAAGGGG 1071

Qy        181 GAACCAGGCCAAGGGCTCAGAGGCTTACAGGGCCCCCCTGGAAAGTTGGGGCCTCCAGGA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1072 GAACCAGGCCAAGGGCTCAGAGGCTTACAGGGCCCCCCTGGAAAGTTGGGGCCTCCAGGA 1131

Qy        241 AATCCAGGGCCTTCTGGGTCACCAGGACCAAAGGGCCAAAAAGGAGACCCTGGAAAAAGT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1132 AATCCAGGGCCTTCTGGGTCACCAGGACCAAAGGGCCAAAAAGGAGACCCTGGAAAAAGT 1191

Qy        301 CCGGATGGTGATAGTAGCCTGGCTGCCTCAGAAAGAAAAGCTCTGCAAACAGAAATGGCA 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1192 CCGGATGGTGATAGTAGCCTGGCTGCCTCAGAAAGAAAAGCTCTGCAAACAGAAATGGCA 1251

Qy        361 CGTATCAAAAAGTGGCTGACCTTCTCTCTCTGGGCAAACAAGTTGGGAACAAGTTCTTCCTG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1252 CGTATCAAAAAGTGGCTGACCTTCTCTCTCTGGGCAAACAAGTTGGGAACAAGTTCTTCCTG 1311

Qy        421 ACCAATGGTGAAATAATGACCTTTGAAAAAGTGAAGGCCTTGTGTGTCAAGTTCCAGGCC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1312 ACCAATGGTGAAATAATGACCTTTGAAAAAGTGAAGGCCTTGTGTGTCAAGTTCCAGGCC 1371

Qy        481 TCTGTGGCCACCCCCAGGAATGCTGCAGAGAATGGAGCCATTCAGAATCTCATCAAGGAG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1372 TCTGTGGCCACCCCCAGGAATGCTGCAGAGAATGGAGCCATTCAGAATCTCATCAAGGAG 1431

Qy        541 GAAGCCTTCCTGGGCATCACTGATGAGAAGACAGAAGGGCAGTTTGTGGATCTGACAGGA 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1432 GAAGCCTTCCTGGGCATCACTGATGAGAAGACAGAAGGGCAGTTTGTGGATCTGACAGGA 1491

Qy        601 AATAGACTGACCTACACAAACTGGAACGAGGGTGAACCCAACAATGCTGGTTCTGATGAA 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1492 AATAGACTGACCTACACAAACTGGAACGAGGGTGAACCCAACAATGCTGGTTCTGATGAA 1551

Qy        661 GATTGTGTATTGCTACTGAAAAATGGCCAGTGGAATGACGTCCCCTGCTCCACCTCCCAT 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1552 GATTGTGTATTGCTACTGAAAAATGGCCAGTGGAATGACGTCCCCTGCTCCACCTCCCAT 1611
```

```
Qy        721 CTGGCCGTCTGTGAGTTCCCTATCTGA 747
              |||||||||||||||||||||||||||
Db       1612 CTGGCCGTCTGTGAGTTCCCTATCTGA 1638


RESULT 9
HOSA16580
LOCUS       HOSA16580               1638 bp    DNA     linear   PRI 17-SEP-1999
DEFINITION  Homo sapiens gene encoding mannan/mannose-binding protein, variant
            LXPA.
ACCESSION   Y16580
VERSION     Y16580.1  GI:5911797
KEYWORDS    mannose-binding lectin; mbl gene.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Madsen,H.O., Satz,M.L., Hogh,B., Svejgaard,A. and Garred,P.
  TITLE     Different molecular events result in low protein levels of
            mannan-binding lectin in populations from southeast Africa and
            South America
  JOURNAL   J. Immunol. 161 (6), 3169-3175 (1998)
  MEDLINE   98414317
   PUBMED   9743385
REFERENCE   2  (bases 1 to 1638)
  AUTHORS   Madsen,H.O.
  TITLE     Direct Submission
  JOURNAL   Submitted (16-FEB-1998) H.O. Madsen, Department of Clinical
            Immunology, Section 7631, National University Hospital, Tagensvej
            20, DK-2200 Copenhagen, DENMARK
COMMENT     Related sequences  X15954, X15955, X15956, X15422.
FEATURES             Location/Qualifiers
     source          1. .1638
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
                     /chromosome="10"
                     /map="10q11.2-q21"
                     /note="MBL haplotype LXPA"
     variation       273
                     /note="polymorphism in different MBL haplotypes"
     variation       396
                     /note="polymorphism in different MBL haplotypes"
     variation       474
                     /note="polymorphism in different MBL haplotypes"
     variation       487
                     /note="polymorphism in different MBL haplotypes"
     variation       495. .500
                     /note="polymorphism in different MBL haplotypes"
     variation       602
                     /note="polymorphism in different MBL haplotypes"
     gene            745. .1638
                     /gene="MBL"
     CAAT_signal     745. .750
                     /gene="MBL"
     variation       753
                     /gene="MBL"
                     /note="polymorphism in different MBL haplotypes"
     TATA_signal     786. .791
                     /gene="MBL"
     mRNA            823. .>1638
                     /gene="MBL"
                     /product="mannose-binding lectin"
     variation       826
                     /gene="MBL"
                     /note="polymorphism in different MBL haplotypes"
     CDS             892. .1638
                     /gene="MBL"
                     /codon_start=1
                     /product="mannose-binding lectin"
                     /protein_id="CAB56122.1"
                     /db_xref="GI:5911798"
                     /db_xref="GOA:P11226"
                     /db_xref="UniProt/Swiss-Prot:P11226"
                     /translation="MSLFPSLPLLLLSMVAASYSETVTCEDAQKTCPAVIACSSPGIN
                     GFPGKDGRDGTKGEKGEPGQGLRGLQGPPGKLGPPGNPGPSGSPGPKGQKGDPGKSPD
                     GDSSLAASERKALQTEMARIKKWLTFSLGKQVGNKFFLTNGEIMTFEKVKALCVKFQA
                     SVATPRNAAENGAIQNLIKEEAFLGITDEKTEGQFVDLTGNRLTYTNWNEGEPNNAGS
                     DEDCVLLLKNGQWNDVPCSTSHLAVCEFPI"
     sig_peptide     892. .951
                     /gene="MBL"
     variation       1045
                     /gene="MBL"
                     /note="polymorphism in different MBL haplotypes"
     variation       1052
                     /gene="MBL"
                     /note="polymorphism in different MBL haplotypes"
     variation       1061
                     /gene="MBL"
                     /note="polymorphism in different MBL haplotypes"
ORIGIN

  Query Match             100.0%;  Score 747;  DB 9;  Length 1638;
  Best Local Similarity   100.0%;  Pred. No. 8.2e-209;
  Matches  747;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATGTCCCTGTTTCCATCACTCCCTCTCCTTCTCCTGAGTATGGTGGCAGCGTCTTACTCA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        892 ATGTCCCTGTTTCCATCACTCCCTCTCCTTCTCCTGAGTATGGTGGCAGCGTCTTACTCA 951

Qy         61 GAAACTGTGACCTGTGAGGATGCCCAAAAGACCTGCCCTGCAGTGATTGCCTGTAGCTCT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        952 GAAACTGTGACCTGTGAGGATGCCCAAAAGACCTGCCCTGCAGTGATTGCCTGTAGCTCT 1011

Qy        121 CCAGGCATCAACGGCTTCCCAGGCAAAGATGGGCGTGATGGCACCAAGGGAGAAAAGGGG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1012 CCAGGCATCAACGGCTTCCCAGGCAAAGATGGGCGTGATGGCACCAAGGGAGAAAAGGGG 1071

Qy        181 GAACCAGGCCAAGGGCTCAGAGGCTTACAGGGCCCCCCTGGAAAGTTGGGGCCTCCAGGA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1072 GAACCAGGCCAAGGGCTCAGAGGCTTACAGGGCCCCCCTGGAAAGTTGGGGCCTCCAGGA 1131

Qy        241 AATCCAGGGCCTTCTGGGTCACCAGGACCAAAGGGCCAAAAAGGAGACCCTGGAAAAAGT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1132 AATCCAGGGCCTTCTGGGTCACCAGGACCAAAGGGCCAAAAAGGAGACCCTGGAAAAAGT 1191

Qy        301 CCGGATGGTGATAGTAGCCTGGCTGCCTCAGAAAGAAAAGCTCTGCAAACAGAAATGGCA 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1192 CCGGATGGTGATAGTAGCCTGGCTGCCTCAGAAAGAAAAGCTCTGCAAACAGAAATGGCA 1251

Qy        361 CGTATCAAAAAGTGGCTGACCTTCTCTCTGGGCAAACAAGTTGGGAACAAGTTCTTCCTG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1252 CGTATCAAAAAGTGGCTGACCTTCTCTCTGGGCAAACAAGTTGGGAACAAGTTCTTCCTG 1311

Qy        421 ACCAATGGTGAAATAATGACCTTTGAAAAAGTGAAGGCCTTGTGTGTCAAGTTCCAGGCC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1312 ACCAATGGTGAAATAATGACCTTTGAAAAAGTGAAGGCCTTGTGTGTCAAGTTCCAGGCC 1371

Qy        481 TCTGTGGCCACCCCCAGGAATGCTGCAGAGAATGGAGCCATTCAGAATCTCATCAAGGAG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1372 TCTGTGGCCACCCCCAGGAATGCTGCAGAGAATGGAGCCATTCAGAATCTCATCAAGGAG 1431

Qy        541 GAAGCCTTCCTGGGCATCACTGATGAGAAGACAGAAGGGCAGTTTGTGGATCTGACAGGA 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1432 GAAGCCTTCCTGGGCATCACTGATGAGAAGACAGAAGGGCAGTTTGTGGATCTGACAGGA 1491

Qy        601 AATAGACTGACCTACACAAACTGGAACGAGGGTGAACCCAACAATGCTGGTTCTGATGAA 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1492 AATAGACTGACCTACACAAACTGGAACGAGGGTGAACCCAACAATGCTGGTTCTGATGAA 1551

Qy        661 GATTGTGTATTGCTACTGAAAAATGGCCAGTGGAATGACGTCCCCTGCTCCACCTCCCAT 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1552 GATTGTGTATTGCTACTGAAAAATGGCCAGTGGAATGACGTCCCCTGCTCCACCTCCCAT 1611

Qy        721 CTGGCCGTCTGTGAGTTCCCTATCTGA 747
```

```
                    ||||||||||||||||||||||||||
Db       1612 CTGGCCGTCTGTGAGTTCCCTATCTGA 1638


RESULT 10
HOSA16581
LOCUS       HOSA16581               1638 bp    DNA     linear   PRI 17-SEP-1999
DEFINITION  Homo sapiens gene encoding mannan/mannose-binding protein, variant
            HYPA.
ACCESSION   Y16581
VERSION     Y16581.1  GI:5911806
KEYWORDS    mannose-binding lectin; mbl gene.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Madsen,H.O., Satz,M.L., Hogh,B., Svejgaard,A. and Garred,P.
  TITLE     Different molecular events result in low protein levels of
            mannan-binding lectin in populations from southeast Africa and
            South America
  JOURNAL   J. Immunol. 161 (6), 3169-3175 (1998)
  MEDLINE   98414317
   PUBMED   9743385
REFERENCE   2  (bases 1 to 1638)
  AUTHORS   Madsen,H.O.
  TITLE     Direct Submission
  JOURNAL   Submitted (16-FEB-1998) H.O. Madsen, Department of Clinical
            Immunology, Section 7631, National University Hospital, Tagensvej
            20, DK-2200 Copenhagen, DENMARK
COMMENT     Related sequences  X15954, X15955, X15956, X15422.
FEATURES             Location/Qualifiers
     source          1. .1638
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
                     /chromosome="10"
                     /map="10q11.2-q21"
                     /note="MBL haplotype HYPA"
     variation       273
                     /note="polymorphism in different MBL haplotypes"
     variation       396
                     /note="polymorphism in different MBL haplotypes"
     variation       474
                     /note="polymorphism in different MBL haplotypes"
     variation       487
                     /note="polymorphism in different MBL haplotypes"
     variation       495. .500
                     /note="polymorphism in different MBL haplotypes"
     variation       602
                     /note="polymorphism in different MBL haplotypes"
     gene            745. .1638
                     /gene="MBL"
     CAAT_signal     745. .750
                     /gene="MBL"
     variation       753
                     /gene="MBL"
                     /note="polymorphism in different MBL haplotypes"
     TATA_signal     786. .791
                     /gene="MBL"
     mRNA            823. .>1638
                     /gene="MBL"
                     /product="mannose-binding lectin"
     variation       826
                     /gene="MBL"
                     /note="polymorphism in different MBL haplotypes"
     CDS             892. .1638
                     /gene="MBL"
                     /codon_start=1
                     /product="mannose-binding lectin"
                     /protein_id="CAB56123.1"
                     /db_xref="GI:5911807"
                     /db_xref="GOA:P11226"
                     /db_xref="UniProt/Swiss-Prot:P11226"
                     /translation="MSLFPSLPLLLLSMVAASYSETVTCEDAQKTCPAVIACSSPGIN
                     GFPGKDGRDGTKGEKGEPGQGLRGLQGPPGKLGPPGNPGPSGSPGPKGQKGDPGKSPD
                     GDSSLAASERKALQTEMARIKKWLTFSLGKQVGNKFFLTNGEIMTFEKVKALCVKFQA
                     SVATPRNAAENGAIQNLIKEEAFLGITDEKTEGQFVDLTGNRLTYTNWNEGEPNNAGS
                     DEDCVLLLKNGQWNDVPCSTSHLAVCEFPI"
     sig_peptide     892. .951
                     /gene="MBL"
     variation       1045
                     /gene="MBL"
                     /note="polymorphism in different MBL haplotypes"
     variation       1052
                     /gene="MBL"
                     /note="polymorphism in different MBL haplotypes"
     variation       1061
                     /gene="MBL"
                     /note="polymorphism in different MBL haplotypes"
ORIGIN

  Query Match             100.0%;  Score 747;  DB 9;  Length 1638;
  Best Local Similarity   100.0%;  Pred. No. 8.2e-209;
  Matches  747;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATGTCCCTGTTTCCATCACTCCCTCTCCTTCTCCTGAGTATGGTGGCAGCGTCTTACTCA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        892 ATGTCCCTGTTTCCATCACTCCCTCTCCTTCTCCTGAGTATGGTGGCAGCGTCTTACTCA 951

Qy         61 GAAACTGTGACCTGTGAGGATGCCCAAAAGACCTGCCCTGCAGTGATTGCCTGTAGCTCT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        952 GAAACTGTGACCTGTGAGGATGCCCAAAAGACCTGCCCTGCAGTGATTGCCTGTAGCTCT 1011

Qy        121 CCAGGCATCAACGGCTTCCCAGGCAAAGATGGGCGTGATGGCACCAAGGGAGAAAAGGGG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1012 CCAGGCATCAACGGCTTCCCAGGCAAAGATGGGCGTGATGGCACCAAGGGAGAAAAGGGG 1071

Qy        181 GAACCAGGCCAAGGGCTCAGAGGCTTACAGGGCCCCCCTGGAAAGTTGGGGCCTCCAGGA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1072 GAACCAGGCCAAGGGCTCAGAGGCTTACAGGGCCCCCCTGGAAAGTTGGGGCCTCCAGGA 1131

Qy        241 AATCCAGGGCCTTCTGGGTCACCAGGACCAAAGGGCCAAAAAGGAGACCCTGGAAAAAGT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1132 AATCCAGGGCCTTCTGGGTCACCAGGACCAAAGGGCCAAAAAGGAGACCCTGGAAAAAGT 1191

Qy        301 CCGGATGGTGATAGTAGCCTGGCTGCCTCAGAAAGAAAAGCTCTGCAAACAGAAATGGCA 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1192 CCGGATGGTGATAGTAGCCTGGCTGCCTCAGAAAGAAAAGCTCTGCAAACAGAAATGGCA 1251

Qy        361 CGTATCAAAAAGTGGCTGACCTTCTCTCTGGGCAAACAAGTTGGGAACAAGTTCTTCCTG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1252 CGTATCAAAAAGTGGCTGACCTTCTCTCTGGGCAAACAAGTTGGGAACAAGTTCTTCCTG 1311

Qy        421 ACCAATGGTGAAATAATGACCTTTGAAAAAGTGAAGGCCTTGTGTGTCAAGTTCCAGGCC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1312 ACCAATGGTGAAATAATGACCTTTGAAAAAGTGAAGGCCTTGTGTGTCAAGTTCCAGGCC 1371

Qy        481 TCTGTGGCCACCCCCAGGAATGCTGCAGAGAATGGAGCCATTCAGAATCTCATCAAGGAG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1372 TCTGTGGCCACCCCCAGGAATGCTGCAGAGAATGGAGCCATTCAGAATCTCATCAAGGAG 1431

Qy        541 GAAGCCTTCCTGGGCATCACTGATGAGAAGACAGAAGGGCAGTTTGTGGATCTGACAGGA 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1432 GAAGCCTTCCTGGGCATCACTGATGAGAAGACAGAAGGGCAGTTTGTGGATCTGACAGGA 1491

Qy        601 AATAGACTGACCTACACAAACTGGAACGAGGGTGAACCCAACAATGCTGGTTCTGATGAA 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1492 AATAGACTGACCTACACAAACTGGAACGAGGGTGAACCCAACAATGCTGGTTCTGATGAA 1551

Qy        661 GATTGTGTATTGCTACTGAAAAATGGCCAGTGGAATGACGTCCCCTGCTCCACCTCCCAT 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1552 GATTGTGTATTGCTACTGAAAAATGGCCAGTGGAATGACGTCCCCTGCTCCACCTCCCAT 1611

Qy        721 CTGGCCGTCTGTGAGTTCCCTATCTGA 747
              |||||||||||||||||||||||||||
```

```
Db       1612 CTGGCCGTCTGTGAGTTCCCTATCTGA 1638


RESULT 11
E27636
LOCUS       E27636                  3605 bp    DNA     linear   PAT 18-JUN-2001
DEFINITION  Recombinant human mannan binding protein and process for producing
            the same.
ACCESSION   E27636
VERSION     E27636.1  GI:13018238
KEYWORDS    JP 1999206378-A/1.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 3605)
  AUTHORS   Nobutaka,W.
  TITLE     Recombinant human mannan binding protein and process for producing
            the same
  JOURNAL   Patent: JP 1999206378-A 1 03-AUG-1999;
            FUSO YAKUHIN KOGYO KK
COMMENT     OS   Homo sapiens
            PN   JP 1999206378-A/1
            PD   03-AUG-1999
            PF   23-JAN-1998 JP 1998011864
            PR
            PI   NOBUTAKA WAKAMIYA
            PC   C12N15/09,C07K14/47,C12P21/02//A61K38/00,(C12N15/09,C12R1:91),
            PC   (C12P21/02,C12R1:91),C12N15/00,A61K37/02,(C12N15/00,C12R1:91)
            CC   Strandedness: Double;
            CC   Topology: Linear;
            FH   Key             Location/Qualifiers
            FT   sig peptide     66. .125
            FT   CDS             66. .812.
FEATURES             Location/Qualifiers
     source          1. .3605
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
ORIGIN

  Query Match             100.0%;  Score 747;  DB 6;  Length 3605;
  Best Local Similarity   100.0%;  Pred. No. 9.1e-209;
  Matches  747;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATGTCCCTGTTTCCATCACTCCCTCTCCTTCTCCTGAGTATGGTGGCAGCGTCTTACTCA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         66 ATGTCCCTGTTTCCATCACTCCCTCTCCTTCTCCTGAGTATGGTGGCAGCGTCTTACTCA 125

Qy         61 GAAACTGTGACCTGTGAGGATGCCCAAAAGACCTGCCCTGCAGTGATTGCCTGTAGCTCT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        126 GAAACTGTGACCTGTGAGGATGCCCAAAAGACCTGCCCTGCAGTGATTGCCTGTAGCTCT 185

Qy        121 CCAGGCATCAACGGCTTCCCAGGCAAAGATGGGCGTGATGGCACCAAGGGAGAAAAGGGG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        186 CCAGGCATCAACGGCTTCCCAGGCAAAGATGGGCGTGATGGCACCAAGGGAGAAAAGGGG 245

Qy        181 GAACCAGGCCAAGGGCTCAGAGGCTTACAGGGCCCCCCTGGAAAGTTGGGGCCTCCAGGA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        246 GAACCAGGCCAAGGGCTCAGAGGCTTACAGGGCCCCCCTGGAAAGTTGGGGCCTCCAGGA 305

Qy        241 AATCCAGGGCCTTCTGGGTCACCAGGACCAAAGGGCCAAAAAGGAGACCCTGGAAAAAGT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        306 AATCCAGGGCCTTCTGGGTCACCAGGACCAAAGGGCCAAAAAGGAGACCCTGGAAAAAGT 365

Qy        301 CCGGATGGTGATAGTAGCCTGGCTGCCTCAGAAAGAAAAGCTCTGCAAACAGAAATGGCA 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        366 CCGGATGGTGATAGTAGCCTGGCTGCCTCAGAAAGAAAAGCTCTGCAAACAGAAATGGCA 425

Qy        361 CGTATCAAAAAGTGGCTGACCTTCTCTCTGGGCAAACAAGTTGGGAACAAGTTCTTCCTG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        426 CGTATCAAAAAGTGGCTGACCTTCTCTCTGGGCAAACAAGTTGGGAACAAGTTCTTCCTG 485

Qy        421 ACCAATGGTGAAATAATGACCTTTGAAAAAGTGAAGGCCTTGTGTGTCAAGTTCCAGGCC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        486 ACCAATGGTGAAATAATGACCTTTGAAAAAGTGAAGGCCTTGTGTGTCAAGTTCCAGGCC 545

Qy        481 TCTGTGGCCACCCCCAGGAATGCTGCAGAGAATGGAGCCATTCAGAATCTCATCAAGGAG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        546 TCTGTGGCCACCCCCAGGAATGCTGCAGAGAATGGAGCCATTCAGAATCTCATCAAGGAG 605

Qy        541 GAAGCCTTCCTGGGCATCACTGATGAGAAGACAGAAGGGCAGTTTGTGGATCTGACAGGA 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        606 GAAGCCTTCCTGGGCATCACTGATGAGAAGACAGAAGGGCAGTTTGTGGATCTGACAGGA 665

Qy        601 AATAGACTGACCTACACAAACTGGAACGAGGGTGAACCCAACAATGCTGGTTCTGATGAA 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        666 AATAGACTGACCTACACAAACTGGAACGAGGGTGAACCCAACAATGCTGGTTCTGATGAA 725

Qy        661 GATTGTGTATTGCTACTGAAAAATGGCCAGTGGAATGACGTCCCCTGCTCCACCTCCCAT 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        726 GATTGTGTATTGCTACTGAAAAATGGCCAGTGGAATGACGTCCCCTGCTCCACCTCCCAT 785

Qy        721 CTGGCCGTCTGTGAGTTCCCTATCTGA 747
              |||||||||||||||||||||||||||
Db        786 CTGGCCGTCTGTGAGTTCCCTATCTGA 812


RESULT 12
AX411061
LOCUS       AX411061                3605 bp    DNA     linear   PAT 14-JUN-2002
DEFINITION  Sequence 3708 from Patent WO0229103.
ACCESSION   AX411061
VERSION     AX411061.1  GI:21443766
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Alvares,C., Horne,D., Peres-da-Silva,S. and Vockley,J.G.
  TITLE     Gene expression profiles in liver cancer
  JOURNAL   Patent: WO 0229103-A 3708 11-APR-2002;
            GENE LOGIC INC (US)
FEATURES             Location/Qualifiers
     source          1. .3605
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
                     /note="EMBL/GenBank Accession No. X15422"
ORIGIN

  Query Match             100.0%;  Score 747;  DB 6;  Length 3605;
  Best Local Similarity   100.0%;  Pred. No. 9.1e-209;
  Matches  747;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATGTCCCTGTTTCCATCACTCCCTCTCCTTCTCCTGAGTATGGTGGCAGCGTCTTACTCA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         66 ATGTCCCTGTTTCCATCACTCCCTCTCCTTCTCCTGAGTATGGTGGCAGCGTCTTACTCA 125

Qy         61 GAAACTGTGACCTGTGAGGATGCCCAAAAGACCTGCCCTGCAGTGATTGCCTGTAGCTCT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        126 GAAACTGTGACCTGTGAGGATGCCCAAAAGACCTGCCCTGCAGTGATTGCCTGTAGCTCT 185

Qy        121 CCAGGCATCAACGGCTTCCCAGGCAAAGATGGGCGTGATGGCACCAAGGGAGAAAAGGGG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        186 CCAGGCATCAACGGCTTCCCAGGCAAAGATGGGCGTGATGGCACCAAGGGAGAAAAGGGG 245

Qy        181 GAACCAGGCCAAGGGCTCAGAGGCTTACAGGGCCCCCCTGGAAAGTTGGGGCCTCCAGGA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        246 GAACCAGGCCAAGGGCTCAGAGGCTTACAGGGCCCCCCTGGAAAGTTGGGGCCTCCAGGA 305

Qy        241 AATCCAGGGCCTTCTGGGTCACCAGGACCAAAGGGCCAAAAAGGAGACCCTGGAAAAAGT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        306 AATCCAGGGCCTTCTGGGTCACCAGGACCAAAGGGCCAAAAAGGAGACCCTGGAAAAAGT 365
```

```
Qy        301 CCGGATGGTGATAGTAGCCTGGCTGCCTCAGAAAGAAAAGCTCTGCAAACAGAAATGGCA 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        366 CCGGATGGTGATAGTAGCCTGGCTGCCTCAGAAAGAAAAGCTCTGCAAACAGAAATGGCA 425

Qy        361 CGTATCAAAAAGTGGCTGACCTTCTCTCTCTGGGCAAACAAGTTGGGAACAAGTTCTTCCTG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        426 CGTATCAAAAAGTGGCTGACCTTCTCTCTCTGGGCAAACAAGTTGGGAACAAGTTCTTCCTG 485

Qy        421 ACCAATGGTGAAATAATGACCTTTGAAAAAGTGAAGGCCTTGTGTGTCAAGTTCCAGGCC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        486 ACCAATGGTGAAATAATGACCTTTGAAAAAGTGAAGGCCTTGTGTGTCAAGTTCCAGGCC 545

Qy        481 TCTGTGGCCACCCCCAGGAATGCTGCAGAGAATGGAGCCATTCAGAATCTCATCAAGGAG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        546 TCTGTGGCCACCCCCAGGAATGCTGCAGAGAATGGAGCCATTCAGAATCTCATCAAGGAG 605

Qy        541 GAAGCCTTCCTGGGCATCACTGATGAGAAGACAGAAGGGCAGTTTGTGGATCTGACAGGA 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        606 GAAGCCTTCCTGGGCATCACTGATGAGAAGACAGAAGGGCAGTTTGTGGATCTGACAGGA 665

Qy        601 AATAGACTGACCTACACAAACTGGAACGAGGGTGAACCCAACAATGCTGGTTCTGATGAA 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        666 AATAGACTGACCTACACAAACTGGAACGAGGGTGAACCCAACAATGCTGGTTCTGATGAA 725

Qy        661 GATTGTGTATTGCTACTGAAAAATGGCCAGTGGAATGACGTCCCCTGCTCCACCTCCCAT 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        726 GATTGTGTATTGCTACTGAAAAATGGCCAGTGGAATGACGTCCCCTGCTCCACCTCCCAT 785

Qy        721 CTGGCCGTCTGTGAGTTCCCTATCTGA 747
              ||||||||||||||||||||||||||
Db        786 CTGGCCGTCTGTGAGTTCCCTATCTGA 812
```

RESULT 13
HSMBPC
LOCUS HSMBPC 3605 bp mRNA linear PRI 31-MAR-1995
DEFINITION Human mRNA for mannose-binding protein C.
ACCESSION X15422
VERSION X15422.1 GI:34486
KEYWORDS mannose-binding protein.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 3605)
AUTHORS Sastry,K., Herman,G.A., Day,L., Deignan,E., Bruns,G., Morton,C.C. and Ezekowitz,R.A.
TITLE The human mannose-binding protein gene. Exon structure reveals its evolutionary relationship to a human pulmonary surfactant gene and localization to chromosome 10
JOURNAL J. Exp. Med. 170 (4), 1175-1189 (1989)
MEDLINE 90010778
PUBMED 2477486
REFERENCE 2 (bases 1 to 3605)
AUTHORS Ezekowitz,R.A.B.
TITLE Direct Submission
JOURNAL Submitted (17-AUG-1989) Ezekowitz R.A.B., The Children's Hospital, Enders Building 7th Floor, 300 Longwood Avenue, Boston MA 02115, U S A
COMMENT X15422 revises MBP cDNA seq published by:
Ezekowitz et. al. J. Exp. Med. 167:1034-1046(1988). Data kindly reviewed (22-FEB-1990) by Ezekowitz R.A.B.
FEATURES Location/Qualifiers
source 1. .3605
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/chromosome="10q11.2-q21."
/clone="48-11"
/cell_line="Hep62"
/cell_type="heatocytes"
/tissue_type="liver"
/clone_lib="lambda gt10"
CDS 66. .812
/codon_start=1
/product="precursor protein"
/protein_id="CAA33462.1"
/db_xref="GI:34487"
/db_xref="GOA:P11226"
/db_xref="UniProt/Swiss-Prot:P11226"
/translation="MSLFPSLPLLLLSMVAASYSETVTCEDAQKTCPAVIACSSPGIN GFPGKDGRDGTKGEKGEPGQGLRGLQGPPGKLGPPGNPGPSGSPGPKGQKGDPGKSPD GDSSLAASERKALQTEMARIKKWLTFSLGKQVGNKFFLTNGEIMTFEKVKALCVKFQA SVATPRNAAENGAIQNLIKEEAFLGITDEKTEGQFVDLTGNRLTYTNWNEGEPNNAGS DEDCVLLLKNGQWNDVPCSTSHLAVCEFPI"
sig_peptide 66. .125
/note="signal peptide (AA -20 to -1)"
mat_peptide 126. .809
/product="mat. mannose-binding protein C (AA 1-228)"
ORIGIN

Query Match 100.0%; Score 747; DB 9; Length 3605;
Best Local Similarity 100.0%; Pred. No. 9.1e-209;
Matches 747; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 ATGTCCCTGTTTCCATCACTCCCTCTCCTTCTCCTGAGTATGGTGGCAGCGTCTTACTCA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         66 ATGTCCCTGTTTCCATCACTCCCTCTCCTTCTCCTGAGTATGGTGGCAGCGTCTTACTCA 125

Qy         61 GAAACTGTGACCTGTGAGGATGCCCAAAAGACCTGCCCTGCAGTGATTGCCTGTAGCTCT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        126 GAAACTGTGACCTGTGAGGATGCCCAAAAGACCTGCCCTGCAGTGATTGCCTGTAGCTCT 185

Qy        121 CCAGGCATCAACGGCTTCCCAGGCAAAGATGGGCGTGATGGCACCAAGGGAGAAAAGGGG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        186 CCAGGCATCAACGGCTTCCCAGGCAAAGATGGGCGTGATGGCACCAAGGGAGAAAAGGGG 245

Qy        181 GAACCAGGCCAAGGGCTCAGAGGCTTACAGGGCCCCCCTGGAAAGTTGGGGCCTCCAGGA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        246 GAACCAGGCCAAGGGCTCAGAGGCTTACAGGGCCCCCCTGGAAAGTTGGGGCCTCCAGGA 305

Qy        241 AATCCAGGGCCTTCTGGGTCACCAGGACCAAAGGGCCAAAAAGGAGACCCTGGAAAAAGT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        306 AATCCAGGGCCTTCTGGGTCACCAGGACCAAAGGGCCAAAAAGGAGACCCTGGAAAAAGT 365

Qy        301 CCGGATGGTGATAGTAGCCTGGCTGCCTCAGAAAGAAAAGCTCTGCAAACAGAAATGGCA 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        366 CCGGATGGTGATAGTAGCCTGGCTGCCTCAGAAAGAAAAGCTCTGCAAACAGAAATGGCA 425

Qy        361 CGTATCAAAAAGTGGCTGACCTTCTCTCTCTGGGCAAACAAGTTGGGAACAAGTTCTTCCTG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        426 CGTATCAAAAAGTGGCTGACCTTCTCTCTCTGGGCAAACAAGTTGGGAACAAGTTCTTCCTG 485

Qy        421 ACCAATGGTGAAATAATGACCTTTGAAAAAGTGAAGGCCTTGTGTGTCAAGTTCCAGGCC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        486 ACCAATGGTGAAATAATGACCTTTGAAAAAGTGAAGGCCTTGTGTGTCAAGTTCCAGGCC 545

Qy        481 TCTGTGGCCACCCCCAGGAATGCTGCAGAGAATGGAGCCATTCAGAATCTCATCAAGGAG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        546 TCTGTGGCCACCCCCAGGAATGCTGCAGAGAATGGAGCCATTCAGAATCTCATCAAGGAG 605

Qy        541 GAAGCCTTCCTGGGCATCACTGATGAGAAGACAGAAGGGCAGTTTGTGGATCTGACAGGA 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        606 GAAGCCTTCCTGGGCATCACTGATGAGAAGACAGAAGGGCAGTTTGTGGATCTGACAGGA 665

Qy        601 AATAGACTGACCTACACAAACTGGAACGAGGGTGAACCCAACAATGCTGGTTCTGATGAA 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        666 AATAGACTGACCTACACAAACTGGAACGAGGGTGAACCCAACAATGCTGGTTCTGATGAA 725

Qy        661 GATTGTGTATTGCTACTGAAAAATGGCCAGTGGAATGACGTCCCCTGCTCCACCTCCCAT 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        726 GATTGTGTATTGCTACTGAAAAATGGCCAGTGGAATGACGTCCCCTGCTCCACCTCCCAT 785

Qy        721 CTGGCCGTCTGTGAGTTCCCTATCTGA 747
              ||||||||||||||||||||||||||
Db        786 CTGGCCGTCTGTGAGTTCCCTATCTGA 812
```

```
RESULT 14
BC069338
LOCUS       BC069338                960 bp    mRNA    linear   PRI 19-AUG-2004
DEFINITION  Homo sapiens mannose-binding lectin (protein C) 2, soluble (opsonic
            defect), mRNA (cDNA clone MGC:97022 IMAGE:7262231), complete cds.
ACCESSION   BC069338
VERSION     BC069338.1  GI:46854807
KEYWORDS    MGC.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 960)
  AUTHORS   Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G.,
            Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D.,
            Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K.,
            Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F.,
            Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L.,
            Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L.,
            Scheetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S.,
            Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J.,
            Abramson,R.D., Mullahy,S.J., Bosak,S.A., McEwan,P.J.,
            McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S.,
            Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W.,
            Villalon,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A.,
            Fahey,J., Helton,E., Ketteman,M., Madan,A., Rodrigues,S.,
            Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y.,
            Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D.,
            Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M.,
            Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smailus,D.E.,
            Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.
  TITLE     Generation and initial analysis of more than 15,000 full-length
            human and mouse cDNA sequences
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
   PUBMED   12477932
REFERENCE   2  (bases 1 to 960)
  AUTHORS   Director MGC Project.
  TITLE     Direct Submission
  JOURNAL   Submitted (29-APR-2004) National Institutes of Health, Mammalian
            Gene Collection (MGC), Cancer Genomics Office, National Cancer
            Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
            USA
  REMARK    NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT     Contact: MGC help desk
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Baylor Human Genome Sequencing Center
            cDNA Library Preparation: Baylor Human Genome Sequencing Center
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Baylor College of Medicine Human Genome
            Sequencing Center
            Center code: BCM-HGSC
            Web site: http://www.hgsc.bcm.tmc.edu/cdna/
            Contact: amg@bcm.tmc.edu
            Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Loulseged, H.,
            Kowis, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M., Nanavati,
            A.N., Gibbs, R.A.

            Clone distribution: MGC clone distribution information can be found
            through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
            Series: IRBR Plate: 2 Row: d Column: 9.
FEATURES             Location/Qualifiers
     source          1. .960
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="MGC:97022 IMAGE:7262231"
                     /tissue_type="PCR rescued clones"
                     /clone_lib="NIH_MGC_277"
                     /note="Vector: pPCR-Script Amp SK(+) with reversed insert"
     gene            1. .960
                     /gene="MBL2"
                     /note="synonyms: COLEC1, MBP1, MBL, MBP"
                     /db_xref="LocusID:4153"
                     /db_xref="MIM:154545"
     CDS             51. .797
                     /gene="MBL2"
                     /codon_start=1
                     /product="soluble mannose-binding lectin, precursor"
                     /protein_id="AAH69338.1"
                     /db_xref="GI:46854808"
                     /db_xref="LocusID:4153"
                     /db_xref="MIM:154545"
                     /translation="MSLFPSLPLLLLSMVAASYSETVTCEDAQKTCPAVIACSSPGIN
                     GFPGKDGRDGTKGEKGEPGQGLRGLQGPPGKLGPPGNPGPSGSPGPKGQKGDPGKSPD
                     GDSSLAASERKALQTEMARIKKWLTFSLGKQVGNKFFLTNGEIMTFEKVKALCVKFQA
                     SVATPRNAAENGAIQNLIKEEAFLGITDEKTEGQFVDLTGNRLTYTNWNEGEPNNAGS
                     DEDCVLLLKNGQWNDVPCSTSHLAVCEFPI"
ORIGIN

  Query Match             99.8%;  Score 745.4;  DB 9;  Length 960;
  Best Local Similarity   99.9%;  Pred. No. 2.3e-208;
  Matches  746;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 ATGTCCCTGTTTCCATCACTCCCTCTCCTTCTCCTGAGTATGGTGGCAGCGTCTTACTCA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         51 ATGTCCCTGTTTCCATCACTCCCTCTCCTTCTCCTGAGTATGGTGGCAGCGTCTTACTCA 110

Qy         61 GAAACTGTGACCTGTGAGGATGCCCAAAAGACCTGCCCTGCAGTGATTGCCTGTAGCTCT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        111 GAAACTGTGACCTGTGAGGATGCCCAAAAGACCTGCCCTGCAGTGATTGCCTGTAGCTCT 170

Qy        121 CCAGGCATCAACGGCTTCCCAGGCAAAGATGGGCGTGATGGCACCAAGGGAGAAAAGGGG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        171 CCAGGCATCAACGGCTTCCCAGGCAAAGATGGGCGTGATGGCACCAAGGGAGAAAAGGGG 230

Qy        181 GAACCAGGCCAAGGGCTCAGAGGCTTACAGGGCCCCCCTGGAAAGTTGGGGCCTCCAGGA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        231 GAACCAGGCCAAGGGCTCAGAGGCTTACAGGGCCCCCCTGGAAAGTTGGGGCCTCCAGGA 290

Qy        241 AATCCAGGGCCTTCTGGGTCACCAGGACCAAAGGGCCAAAAAGGAGACCCTGGAAAAAGT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        291 AATCCAGGGCCTTCTGGGTCACCAGGACCAAAGGGCCAAAAAGGAGACCCTGGAAAAAGT 350

Qy        301 CCGGATGGTGATAGTAGCCTGGCTGCCTCAGAAAGAAAAGCTCTGCAAACAGAAATGGCA 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        351 CCGGATGGTGATAGTAGCCTGGCTGCCTCAGAAAGAAAAGCTCTGCAAACAGAAATGGCA 410

Qy        361 CGTATCAAAAAGTGGCTGACCTTCTCTCTGGGCAAACAAGTTGGGAACAAGTTCTTCCTG 420
              |||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||
Db        411 CGTATCAAAAAGTGGCTCACCTTCTCTCTGGGCAAACAAGTTGGGAACAAGTTCTTCCTG 470

Qy        421 ACCAATGGTGAAATAATGACCTTTGAAAAAGTGAAGGCCTTGTGTGTCAAGTTCCAGGCC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        471 ACCAATGGTGAAATAATGACCTTTGAAAAAGTGAAGGCCTTGTGTGTCAAGTTCCAGGCC 530

Qy        481 TCTGTGGCCACCCCCAGGAATGCTGCAGAGAATGGAGCCATTCAGAATCTCATCAAGGAG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        531 TCTGTGGCCACCCCCAGGAATGCTGCAGAGAATGGAGCCATTCAGAATCTCATCAAGGAG 590

Qy        541 GAAGCCTTCCTGGGCATCACTGATGAGAAGACAGAAGGGCAGTTTGTGGATCTGACAGGA 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        591 GAAGCCTTCCTGGGCATCACTGATGAGAAGACAGAAGGGCAGTTTGTGGATCTGACAGGA 650

Qy        601 AATAGACTGACCTACACAAACTGGAACGAGGGTGAACCCAACAATGCTGGTTCTGATGAA 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        651 AATAGACTGACCTACACAAACTGGAACGAGGGTGAACCCAACAATGCTGGTTCTGATGAA 710

Qy        661 GATTGTGTATTGCTACTGAAAAATGGCCAGTGGAATGACGTCCCCTGCTCCACCTCCCAT 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        711 GATTGTGTATTGCTACTGAAAAATGGCCAGTGGAATGACGTCCCCTGCTCCACCTCCCAT 770

Qy        721 CTGGCCGTCTGTGAGTTCCCTATCTGA 747
              |||||||||||||||||||||||||||
Db        771 CTGGCCGTCTGTGAGTTCCCTATCTGA 797
```

```
RESULT 15
CQ875889
LOCUS       CQ875889                1632 bp    DNA     linear   PAT 04-OCT-2004
DEFINITION  Sequence 22 from Patent WO2004065626.
ACCESSION   CQ875889
VERSION     CQ875889.1  GI:53789632
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Garred,P., Madsen,H.O. and str M,J.
  TITLE     A method of sepsis prognosis
  JOURNAL   Patent: WO 2004065626-A 22 05-AUG-2004;
            Rigshospitalet (DK); Kobenhavns Amt (DK)
FEATURES             Location/Qualifiers
     source          1. .1632
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
ORIGIN

  Query Match             99.8%;  Score 745.4;  DB 6;  Length 1632;
  Best Local Similarity   99.9%;  Pred. No. 2.4e-208;
  Matches  746;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 ATGTCCCTGTTTCCATCACTCCCTCTCCTTCTCCTGAGTATGGTGGCAGCGTCTTACTCA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        886 ATGTCCCTGTTTCCATCACTCCCTCTCCTTCTCCTGAGTATGGTGGCAGCGTCTTACTCA 945

Qy         61 GAAACTGTGACCTGTGAGGATGCCCAAAAGACCTGCCCTGCAGTGATTGCCTGTAGCTCT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        946 GAAACTGTGACCTGTGAGGATGCCCAAAAGACCTGCCCTGCAGTGATTGCCTGTAGCTCT 1005

Qy        121 CCAGGCATCAACGGCTTCCCAGGCAAAGATGGGCGTGATGGCACCAAGGGAGAAAAGGGG 180
              |||||||||||||||||||||||||||||||||||||||||||||| ||||||||||
Db       1006 CCAGGCATCAACGGCTTCCCAGGCAAAGATGGGCGTGATGGCACCAAGGAAGAAAAGGGG 1065

Qy        181 GAACCAGGCCAAGGGCTCAGAGGCTTACAGGGCCCCCCTGGAAAGTTGGGGCCTCCAGGA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1066 GAACCAGGCCAAGGGCTCAGAGGCTTACAGGGCCCCCCTGGAAAGTTGGGGCCTCCAGGA 1125

Qy        241 AATCCAGGGCCTTCTGGGTCACCAGGACCAAAGGGCCAAAAAGGAGACCCTGGAAAAAGT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1126 AATCCAGGGCCTTCTGGGTCACCAGGACCAAAGGGCCAAAAAGGAGACCCTGGAAAAAGT 1185

Qy        301 CCGGATGGTGATAGTAGCCTGGCTGCCTCAGAAAGAAAAGCTCTGCAAACAGAAATGGCA 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1186 CCGGATGGTGATAGTAGCCTGGCTGCCTCAGAAAGAAAAGCTCTGCAAACAGAAATGGCA 1245

Qy        361 CGTATCAAAAAGTGGCTGACCTTCTCTCTGGGCAAACAAGTTGGGAACAAGTTCTTCCTG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1246 CGTATCAAAAAGTGGCTGACCTTCTCTCTGGGCAAACAAGTTGGGAACAAGTTCTTCCTG 1305

Qy        421 ACCAATGGTGAAATAATGACCTTTGAAAAAGTGAAGGCCTTGTGTGTCAAGTTCCAGGCC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1306 ACCAATGGTGAAATAATGACCTTTGAAAAAGTGAAGGCCTTGTGTGTCAAGTTCCAGGCC 1365

Qy        481 TCTGTGGCCACCCCCAGGAATGCTGCAGAGAATGGAGCCATTCAGAATCTCATCAAGGAG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1366 TCTGTGGCCACCCCCAGGAATGCTGCAGAGAATGGAGCCATTCAGAATCTCATCAAGGAG 1425

Qy        541 GAAGCCTTCCTGGGCATCACTGATGAGAAGACAGAAGGGCAGTTTGTGGATCTGACAGGA 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1426 GAAGCCTTCCTGGGCATCACTGATGAGAAGACAGAAGGGCAGTTTGTGGATCTGACAGGA 1485

Qy        601 AATAGACTGACCTACACAAACTGGAACGAGGGTGAACCCAACAATGCTGGTTCTGATGAA 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1486 AATAGACTGACCTACACAAACTGGAACGAGGGTGAACCCAACAATGCTGGTTCTGATGAA 1545

Qy        661 GATTGTGTATTGCTACTGAAAAATGGCCAGTGGAATGACGTCCCCTGCTCCACCTCCCAT 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1546 GATTGTGTATTGCTACTGAAAAATGGCCAGTGGAATGACGTCCCCTGCTCCACCTCCCAT 1605

Qy        721 CTGGCCGTCTGTGAGTTCCCTATCTGA 747
              |||||||||||||| ||||||||||||
Db       1606 CTGGCCGTCTGTGAGTTCCCTATCTGA 1632


Search completed: June 20, 2005, 17:02:04
Job time : 3608 secs
```

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 19, 2005, 14:00:45 ; Search time 541 Seconds
(without alignments)
8173.839 Million cell updates/sec

Title: US-10-054-536-2
Perfect score: 747
Sequence: 1 atgtccctgtttccatcact.....tctgtgagttccctatctga 747

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_16Dec04:*
1: geneseqn1980s:*
2: geneseqn1990s:*
3: geneseqn2000s:*
4: geneseqn2001as:*
5: geneseqn2001bs:*
6: geneseqn2002as:*
7: geneseqn2002bs:*
8: geneseqn2003as:*
9: geneseqn2003bs:*
10: geneseqn2003cs:*
11: geneseqn2003ds:*
12: geneseqn2004as:*
13: geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	747	100.0	747	2	AAZ07142	Aaz07142 Human man
2	747	100.0	747	12	ADI20100	Adi20100 DNA seque
3	747	100.0	900	6	ABK14771	Abk14771 DNA encod
4	747	100.0	1632	13	ADR29055	Adr29055 Human MBL
5	747	100.0	1638	12	ADP03860	Adp03860 Human mbl
6	747	100.0	1638	13	ADR29056	Adr29056 Human MBL
7	747	100.0	1638	13	ADR29059	Adr29059 Human MBL
8	747	100.0	1638	13	ADR29061	Adr29061 Human MBL
9	747	100.0	3605	2	AAZ07143	Aaz07143 Human man
10	747	100.0	3605	6	ABN97210	Abn97210 Gene #370
11	747	100.0	3605	12	ADI20099	Adi20099 DNA seque
12	747	100.0	3605	12	ADJ45526	Adj45526 cDNA enco
13	745.4	99.8	1632	13	ADR29057	Adr29057 Human MBL
14	745.4	99.8	1638	13	ADR29058	Adr29058 Human MBL
15	745.4	99.8	1638	13	ADR29060	Adr29060 Human MBL
16	742.2	99.4	3592	2	AAQ53529	Aaq53529 Human Man
17	734	98.3	1644	12	ADP03848	Adp03848 Human mbl
18	734	98.3	1644	12	ADP03836	Adp03836 Human mbl
19	734	98.3	1644	12	ADP03840	Adp03840 Human mbl
20	734	98.3	1644	12	ADP03844	Adp03844 Human mbl
21	734	98.3	1644	12	ADP03856	Adp03856 Human mbl
22	734	98.3	1644	12	ADP03852	Adp03852 Human mbl
23	684	91.6	684	2	AAX29295	Aax29295 Mannan-bi
24	673.4	90.1	1143	12	ADO21125	Ado21125 Human car
25	635.8	85.1	963	1	AAN91079	Aan91079 cDNA of h
26	444.6	59.5	1409	6	AAD45344	Aad45344 Human ant
27	395	52.9	1010	3	AAA70738	Aaa70738 Pig serum
28	374	50.1	3336	2	AAQ64652	Aaq64652 Human Man
29	364.6	48.8	1037	6	ABK63803	Abk63803 Rat seque
30	364.6	48.8	1037	10	ADB58487	Adb58487 Toxicity-
31	287.6	38.5	1068	12	ADP71919	Adp71919 Renal tox
32	286	38.3	717	10	ADB58066	Adb58066 Toxicity-
33	286	38.3	717	10	ADB52544	Adb52544 Primary r
34	284.4	38.1	943	4	AAH44805	Aah44805 Murine cD
35	280.6	37.6	1437	4	AAK51894	Aak51894 Human pol
c 36	274.4	36.7	1662	4	AAK52878	Aak52878 Human pol
37	240.6	32.2	1248	12	ADP28880	Adp28880 Human sec
c 38	224	30.0	1143	12	ADO21125	Ado21125 Human car
39	222	29.7	419	8	ABX46620	Abx46620 Bovine ES
40	204.4	27.4	1211	6	ABK14789	Abk14789 DNA encod
41	188	25.2	1802	2	AAQ53530	Aaq53530 Human Man
42	186.2	24.9	405	6	ABS66633	Abs66633 Rat PrMBP
43	186	24.9	1802	10	ABX08715	Abx08715 Pathogeni
44	186	24.9	1802	10	ABX08719	Abx08719 Pathogeni
45	186	24.9	1802	10	ABX08711	Abx08711 Pathogeni

ALIGNMENTS

RESULT 1
AAZ07142
ID AAZ07142 standard; cDNA; 747 BP.
XX
AC AAZ07142;
XX
DT 11-OCT-1999 (first entry)
XX
DE Human mannan-binding protein encoding cDNA.
XX
KW Human; mannan-binding protein; hMBP; recombinant; inhibition; infection;
KW rhMBP; haemagglutination; influenza; HIV; primer; ss.
XX
OS Homo sapiens.
XX
PN WO9937676-A1.
XX
PD 29-JUL-1999.
XX
PF 23-JUL-1998; 98WO-JP003311.
XX
PR 23-JAN-1998; 98JP-00011864.
XX
PA (FUSO) FUSO PHARM IND LTD.
XX
PI Wakamiya N;
XX
DR WPI; 1999-469114/39.
DR P-PSDB; AAY29485.
XX
PT Recombinant human mannan-binding protein expressed using pNOW1 vector.
XX
PS Example 2; Page 74; 91pp; Japanese.
XX
CC The present invention describes recombinant human mannan-binding protein
CC (rhMBP) having a molecular weight range of 1000-1300 or 200-400 kDa (by
CC gel filtration with detection at 280 nm). rhMBP may be used as a
CC component of drug compositions for the inhibition of haemagglutination
CC and prevention of infection by viruses such as influenza and HIV. The
CC present sequence encodes hMBP (human mannan-binding protein)
XX
SQ Sequence 747 BP; 203 A; 187 C; 202 G; 155 T; 0 U; 0 Other;

Query Match 100.0%; Score 747; DB 2; Length 747;
Best Local Similarity 100.0%; Pred. No. 1.1e-207;
Matches 747; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 ATGTCCCTGTTTCCATCACTCCCTCTCCTTCTCCTGAGTATGGTGGCAGCGTCTTACTCA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGTCCCTGTTTCCATCACTCCCTCTCCTTCTCCTGAGTATGGTGGCAGCGTCTTACTCA 60

Qy         61 GAAACTGTGACCTGTGAGGATGCCCAAAAGACCTGCCCTGCAGTGATTGCCTGTAGCTCT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GAAACTGTGACCTGTGAGGATGCCCAAAAGACCTGCCCTGCAGTGATTGCCTGTAGCTCT 120

Qy        121 CCAGGCATCAACGGCTTCCCAGGCAAAGATGGGCGTGATGGCACCAAGGGAGAAAAGGGG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CCAGGCATCAACGGCTTCCCAGGCAAAGATGGGCGTGATGGCACCAAGGGAGAAAAGGGG 180

Qy        181 GAACCAGGCCAAGGGCTCAGAGGCTTACAGGGCCCCCCTGGAAAGTTGGGGCCTCCAGGA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GAACCAGGCCAAGGGCTCAGAGGCTTACAGGGCCCCCCTGGAAAGTTGGGGCCTCCAGGA 240

Qy        241 AATCCAGGGCCTTCTGGGTCACCAGGACCAAAGGGCCAAAAAGGAGACCCTGGAAAAAGT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 AATCCAGGGCCTTCTGGGTCACCAGGACCAAAGGGCCAAAAAGGAGACCCTGGAAAAAGT 300

Qy        301 CCGGATGGTGATAGTAGCCTGGCTGCCTCAGAAAGAAAAGCTCTGCAAACAGAAATGGCA 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 CCGGATGGTGATAGTAGCCTGGCTGCCTCAGAAAGAAAAGCTCTGCAAACAGAAATGGCA 360

Qy        361 CGTATCAAAAAGTGGCTGACCTTCTCTCTGGGCAAACAAGTTGGGAACAAGTTCTTCCTG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 CGTATCAAAAAGTGGCTGACCTTCTCTCTGGGCAAACAAGTTGGGAACAAGTTCTTCCTG 420

Qy        421 ACCAATGGTGAAATAATGACCTTTGAAAAAGTGAAGGCCTTGTGTGTCAAGTTCCAGGCC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 ACCAATGGTGAAATAATGACCTTTGAAAAAGTGAAGGCCTTGTGTGTCAAGTTCCAGGCC 480

Qy        481 TCTGTGGCCACCCCCAGGAATGCTGCAGAGAATGGAGCCATTCAGAATCTCATCAAGGAG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 TCTGTGGCCACCCCCAGGAATGCTGCAGAGAATGGAGCCATTCAGAATCTCATCAAGGAG 540

Qy        541 GAAGCCTTCCTGGGCATCACTGATGAGAAGACAGAAGGGCAGTTTGTGGATCTGACAGGA 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GAAGCCTTCCTGGGCATCACTGATGAGAAGACAGAAGGGCAGTTTGTGGATCTGACAGGA 600

Qy        601 AATAGACTGACCTACACAAACTGGAACGAGGGTGAACCCAACAATGCTGGTTCTGATGAA 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 AATAGACTGACCTACACAAACTGGAACGAGGGTGAACCCAACAATGCTGGTTCTGATGAA 660

Qy        661 GATTGTGTATTGCTACTGAAAAATGGCCAGTGGAATGACGTCCCCTGCTCCACCTCCCAT 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 GATTGTGTATTGCTACTGAAAAATGGCCAGTGGAATGACGTCCCCTGCTCCACCTCCCAT 720

Qy        721 CTGGCCGTCTGTGAGTTCCCTATCTGA 747
              |||||||||||||||||||||||||||
Db        721 CTGGCCGTCTGTGAGTTCCCTATCTGA 747
```

RESULT 2
ADI20100
ID ADI20100 standard; DNA; 747 BP.
XX
AC ADI20100;
XX
DT 22-APR-2004 (first entry)
XX
DE DNA sequence #2 related to the invention.
XX
KW anti-human immunodeficiency virus; HIV; mannose binding protein; MBP; ds.
XX
OS Homo sapiens.
XX
PN WO2004002511-A1.
XX
PD 08-JAN-2004.
XX
PF 30-JUN-2003; 2003WO-JP008259.
XX
PR 28-JUN-2002; 2002JP-00189534.
XX
PA (FUSO) FUSO PHARM IND LTD.
XX
PI Wakamiya N, Ohtani K, Sakamoto T, Keshi H, Kishi Y;
XX
DR WPI; 2004-082879/08.
XX
PT Anti-human immunodeficiency virus (HIV) agent comprising a mannose
PT binding protein for treatment of HIV infection.
XX
PS Disclosure; SEQ ID NO 2; 44pp; Japanese.
XX
CC The present invention relates to anti-human immunodeficiency virus (HIV)
CC agent comprises a mannose binding protein (MBP). For use in the treatment
CC of HIV. The present sequence represents a DNA sequence related to the
CC invention.
XX
SQ Sequence 747 BP; 203 A; 187 C; 202 G; 155 T; 0 U; 0 Other;

Query Match 100.0%; Score 747; DB 12; Length 747;
Best Local Similarity 100.0%; Pred. No. 1.1e-207;
Matches 747; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 ATGTCCCTGTTTCCATCACTCCCTCTCCTTCTCCTGAGTATGGTGGCAGCGTCTTACTCA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGTCCCTGTTTCCATCACTCCCTCTCCTTCTCCTGAGTATGGTGGCAGCGTCTTACTCA 60

Qy         61 GAAACTGTGACCTGTGAGGATGCCCAAAAGACCTGCCCTGCAGTGATTGCCTGTAGCTCT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GAAACTGTGACCTGTGAGGATGCCCAAAAGACCTGCCCTGCAGTGATTGCCTGTAGCTCT 120

Qy        121 CCAGGCATCAACGGCTTCCCAGGCAAAGATGGGCGTGATGGCACCAAGGGAGAAAAGGGG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CCAGGCATCAACGGCTTCCCAGGCAAAGATGGGCGTGATGGCACCAAGGGAGAAAAGGGG 180

Qy        181 GAACCAGGCCAAGGGCTCAGAGGCTTACAGGGCCCCCCTGGAAAGTTGGGGCCTCCAGGA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GAACCAGGCCAAGGGCTCAGAGGCTTACAGGGCCCCCCTGGAAAGTTGGGGCCTCCAGGA 240

Qy        241 AATCCAGGGCCTTCTGGGTCACCAGGACCAAAGGGCCAAAAAGGAGACCCTGGAAAAAGT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 AATCCAGGGCCTTCTGGGTCACCAGGACCAAAGGGCCAAAAAGGAGACCCTGGAAAAAGT 300

Qy        301 CCGGATGGTGATAGTAGCCTGGCTGCCTCAGAAAGAAAAGCTCTGCAAACAGAAATGGCA 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 CCGGATGGTGATAGTAGCCTGGCTGCCTCAGAAAGAAAAGCTCTGCAAACAGAAATGGCA 360

Qy        361 CGTATCAAAAAGTGGCTGACCTTCTCTCTGGGCAAACAAGTTGGGAACAAGTTCTTCCTG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 CGTATCAAAAAGTGGCTGACCTTCTCTCTGGGCAAACAAGTTGGGAACAAGTTCTTCCTG 420

Qy        421 ACCAATGGTGAAATAATGACCTTTGAAAAAGTGAAGGCCTTGTGTGTCAAGTTCCAGGCC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 ACCAATGGTGAAATAATGACCTTTGAAAAAGTGAAGGCCTTGTGTGTCAAGTTCCAGGCC 480

Qy        481 TCTGTGGCCACCCCCAGGAATGCTGCAGAGAATGGAGCCATTCAGAATCTCATCAAGGAG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 TCTGTGGCCACCCCCAGGAATGCTGCAGAGAATGGAGCCATTCAGAATCTCATCAAGGAG 540

Qy        541 GAAGCCTTCCTGGGCATCACTGATGAGAAGACAGAAGGGCAGTTTGTGGATCTGACAGGA 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GAAGCCTTCCTGGGCATCACTGATGAGAAGACAGAAGGGCAGTTTGTGGATCTGACAGGA 600

Qy        601 AATAGACTGACCTACACAAACTGGAACGAGGGTGAACCCAACAATGCTGGTTCTGATGAA 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 AATAGACTGACCTACACAAACTGGAACGAGGGTGAACCCAACAATGCTGGTTCTGATGAA 660

Qy        661 GATTGTGTATTGCTACTGAAAAATGGCCAGTGGAATGACGTCCCCTGCTCCACCTCCCAT 720
```

```
Db        661 GATTGTGTATTGCTACTGAAAAATGGCCAGTGGAATGACGTCCCCTGCTCCACCTCCCAT 720

Qy        721 CTGGCCGTCTGTGAGTTCCCTATCTGA 747
              ||||||||||||||||||||||||||||
Db        721 CTGGCCGTCTGTGAGTTCCCTATCTGA 747


RESULT 3
ABK14771
ID   ABK14771 standard; DNA; 900 BP.
XX
AC   ABK14771;
XX
DT   08-MAY-2002  (first entry)
XX
DE   DNA encoding human mannose-binding protein (MBP).
XX
KW   Human; mannose-binding protein; MBP; methylotrophic yeast strain;
KW   protein disulphide isomerase; PDI; heat shock protein 47; hsp47;
KW   propyl-4-hydroxylase; P4H; pathogenic organism disposal; biocide; gene;
KW   ds.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             66. .812
FT                   /*tag=  a
FT                   /product= "Mannose-binding protein (MBP)"
XX
PN   US6337193-B1.
XX
PD   08-JAN-2002.
XX
PF   24-NOV-1998;   98US-00198603.
XX
PR   24-NOV-1998;   98US-00198603.
XX
PA   (APTA-) APTAGEN INC.
XX
PI   Tully RE,  Caltagirone GT,  Moyer SS,  Ronning MT;
XX
DR   WPI; 2002-163238/21.
DR   P-PSDB; AAU75574.
XX
PT   Methylotrophic yeast strain, useful for producing mannose-binding
PT   protein, comprises DNA molecules encoding the protein, protein disulfide
PT   isomerase, heat shock protein 47 and propyl-4-hydroxylase.
XX
PS   Claim 5; Fig 1; 30pp; English.
XX
CC   The invention relates to a methylotrophic yeast strain (I) comprising a
CC   DNA molecule encoding mannose-binding protein (MBP), protein disulphide
CC   isomerase (PDI), heat shock protein 47 (hsp47), and propyl-4-hydroxylase
CC   (P4H), where upon culturing (I) produces the MBP, PDI, hsp47 and P4H. (I)
CC   is useful for producing MBP comprising culturing (I) under conditions
CC   suitable for the secretion of MBP by the yeast where MBP is utilised in
CC   disposal of pathogenic organisms by opsonising pathogen or activating
CC   complement cascade. The methods utilising (I) result in high yields of
CC   MBP without the use of foetal calf serum, in a cost-effective manner. The
CC   present sequence relates to the coding sequence of human mannose-binding
CC   protein
XX
SQ   Sequence 900 BP; 246 A; 225 C; 228 G; 201 T; 0 U; 0 Other;

  Query Match             100.0%;  Score 747;  DB 6;  Length 900;
  Best Local Similarity   100.0%;  Pred. No. 1.2e-207;
  Matches  747;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATGTCCCTGTTTCCATCACTCCCTCTCCTTCTCCTGAGTATGGTGGCAGCGTCTTACTCA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         66 ATGTCCCTGTTTCCATCACTCCCTCTCCTTCTCCTGAGTATGGTGGCAGCGTCTTACTCA 125

Qy         61 GAAACTGTGACCTGTGAGGATGCCCAAAAGACCTGCCCTGCAGTGATTGCCTGTAGCTCT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        126 GAAACTGTGACCTGTGAGGATGCCCAAAAGACCTGCCCTGCAGTGATTGCCTGTAGCTCT 185

Qy        121 CCAGGCATCAACGGCTTCCCAGGCAAAGATGGGCGTGATGGCACCAAGGGAGAAAAGGGG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        186 CCAGGCATCAACGGCTTCCCAGGCAAAGATGGGCGTGATGGCACCAAGGGAGAAAAGGGG 245

Qy        181 GAACCAGGCCAAGGGCTCAGAGGCTTACAGGGCCCCCCTGGAAAGTTGGGGCCTCCAGGA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        246 GAACCAGGCCAAGGGCTCAGAGGCTTACAGGGCCCCCCTGGAAAGTTGGGGCCTCCAGGA 305

Qy        241 AATCCAGGGCCTTCTGGGTCACCAGGACCAAAGGGCCAAAAAGGAGACCCTGGAAAAAGT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        306 AATCCAGGGCCTTCTGGGTCACCAGGACCAAAGGGCCAAAAAGGAGACCCTGGAAAAAGT 365

Qy        301 CCGGATGGTGATAGTAGCCTGGCTGCCTCAGAAAGAAAAGCTCTGCAAACAGAAATGGCA 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        366 CCGGATGGTGATAGTAGCCTGGCTGCCTCAGAAAGAAAAGCTCTGCAAACAGAAATGGCA 425

Qy        361 CGTATCAAAAAGTGGCTGACCTTCTCTCTGGGCAAACAAGTTGGGAACAAGTTCTTCCTG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        426 CGTATCAAAAAGTGGCTGACCTTCTCTCTGGGCAAACAAGTTGGGAACAAGTTCTTCCTG 485

Qy        421 ACCAATGGTGAAATAATGACCTTTGAAAAAGTGAAGGCCTTGTGTGTCAAGTTCCAGGCC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        486 ACCAATGGTGAAATAATGACCTTTGAAAAAGTGAAGGCCTTGTGTGTCAAGTTCCAGGCC 545

Qy        481 TCTGTGGCCACCCCCAGGAATGCTGCAGAGAATGGAGCCATTCAGAATCTCATCAAGGAG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        546 TCTGTGGCCACCCCCAGGAATGCTGCAGAGAATGGAGCCATTCAGAATCTCATCAAGGAG 605

Qy        541 GAAGCCTTCCTGGGCATCACTGATGAGAAGACAGAAGGGCAGTTTGTGGATCTGACAGGA 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        606 GAAGCCTTCCTGGGCATCACTGATGAGAAGACAGAAGGGCAGTTTGTGGATCTGACAGGA 665

Qy        601 AATAGACTGACCTACACAAACTGGAACGAGGGTGAACCCAACAATGCTGGTTCTGATGAA 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        666 AATAGACTGACCTACACAAACTGGAACGAGGGTGAACCCAACAATGCTGGTTCTGATGAA 725

Qy        661 GATTGTGTATTGCTACTGAAAAATGGCCAGTGGAATGACGTCCCCTGCTCCACCTCCCAT 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        726 GATTGTGTATTGCTACTGAAAAATGGCCAGTGGAATGACGTCCCCTGCTCCACCTCCCAT 785

Qy        721 CTGGCCGTCTGTGAGTTCCCTATCTGA 747
              ||||||||||||||||||||||||||||
Db        786 CTGGCCGTCTGTGAGTTCCCTATCTGA 812


RESULT 4
ADR29055
ID   ADR29055 standard; DNA; 1632 BP.
XX
AC   ADR29055;
XX
DT   21-OCT-2004  (first entry)
XX
DE   Human MBL gene with non-structural/variant structural allele (codon 57).
XX
KW   Sepsis; septic shock; severe; MBL; mannose binding lectin; SIRS;
KW   systemic inflammatory response syndrome; innate immune defence;
KW   single nucleotide polymorphism; SNP; structural variant; regulatory;
KW   prophylaxis; sepsis syndrome; infection susceptibility;
KW   multiple organ failure; MOF; multiple organ dysfunction; acute; gene; ds;
KW   human.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   variation       396
FT                   /*tag=  a
FT                   /standard_name= "Single nucleotide polymorphism"
FT                   /note= "Non-structural allele"
```

```
FT   variation       474
FT                   /*tag=  b
FT                   /standard_name= "Single nucleotide polymorphism"
FT                   /note= "Non-structural allele"
FT   variation       487
FT                   /*tag=  c
FT                   /standard_name= "Single nucleotide polymorphism"
FT                   /note= "Non-structural allele"
FT   variation       747
FT                   /*tag=  d
FT                   /standard_name= "Single nucleotide polymorphism"
FT                   /note= "Non-structural allele"
FT   variation       820
FT                   /*tag=  e
FT                   /standard_name= "Single nucleotide polymorphism"
FT                   /note= "Non-structural allele"
FT   variation       1055
FT                   /*tag=  f
FT                   /standard_name= "Single nucleotide polymorphism"
FT                   /note= "Variant structural allele"
XX
PN   WO2004065626-A2.
XX
PD   05-AUG-2004.
XX
PF   16-JAN-2004; 2004WO-DK000027.
XX
PR   17-JAN-2003; 2003DK-00000042.
PR   06-MAR-2003; 2003US-0453272P.
XX
PA   (RIGS-) RIGSHOSPITALET.
PA   (KOBE-) KOBENHAVNS AMT.
XX
PI   Garred P,  Madsen HO,  Strom J;
XX
DR   WPI; 2004-571694/55.
XX
PT   Predicting whether an individual having Systemic Inflammatory Response
PT   Syndrome (SIRS) will develop sepsis, useful for treating sepsis,
PT   comprises determining the mannose-binding lectin (MBL) genotype or
PT   concentration of MBL.
XX
PS   Disclosure; SEQ ID NO 20; 65pp; English.
XX
CC   The invention relates to a method to determine the risk factor of a
CC   person for sepsis, severe sepsis or septic shock by correlating MBL
CC   (mannose binding lectin) genotype with a predefined risk value. It
CC   discloses the connection between the MBL genotype of an individual having
CC   SIRS (Systemic Inflammatory Response Syndrome) and the risk of developing
CC   sepsis, severe sepsis or septic shock. It shows how a decreased level of
CC   MBL and lack of functional MBL are crucial to the development of sepsis
CC   and septic shock in an individual having sepsis. A MBL is an important
CC   factor in innate immune defence. MBL single nucleotide polymorphism in
CC   the form of the structural variant (codon 54, codon 52 and codon 57) and
CC   regulatory variant (low expression and high expression) were studied.
CC   This invention discloses that the MBL gene polymorphism's causes a
CC   reduction of the MBL level, which is associated with the development and
CC   progression of sepsis in adult intensive care patients. The invention
CC   offers a service to determine whether an individual belongs to a risk
CC   group and it provides the treatment accordingly. There is an increased
CC   risk of a fatal outcome of an individual carrying MBL variant alleles. A
CC   rapid determination of MBL genotype of patients is important in
CC   identifying individuals at risk of developing sepsis, severe sepsis or
CC   septic shock. The MBL can be used for a medicament for the prevention and
CC   treatment of specified diseases. The MBL variant allele is also
CC   associated with an increased risk of death. It raises the prospective
CC   that MBL (MBL substitution) can be used in prophylaxis and treatment of
CC   sepsis syndrome. The frequency of MBL variant alleles is proportional to
CC   the severity of sepsis which indicates lacking buffering capacity of MBL
CC   towards initial microbial replication. It is not only associated with
CC   susceptibility of infection but also allows activation of host mechanisms
CC   central to the pathophysiology of the sepsis syndrome. The invention can
CC   also predict the risk for developing multiple organ failure (MOF),
CC   multiple organ dysfunction and acute organ dysfunction of an individual
CC   having SIRS. The high risk is characterised by the presence of at least
CC   one variant structural allele of the MBL gene and or having two low
CC   expression regulatory alleles of the MBL gene in a sample. The presented
CC   sequence is the human MBL gene with non-structural and variant structural
CC   allele (codon 57).
XX
SQ   Sequence 1632 BP; 447 A; 381 C; 430 G; 374 T; 0 U; 0 Other;

  Query Match             100.0%;  Score 747;  DB 13;  Length 1632;
  Best Local Similarity   100.0%;  Pred. No. 1.6e-207;
  Matches  747;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATGTCCCTGTTTCCATCACTCCCTCTCCTTCTCCTGAGTATGGTGGCAGCGTCTTACTCA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        886 ATGTCCCTGTTTCCATCACTCCCTCTCCTTCTCCTGAGTATGGTGGCAGCGTCTTACTCA 945

Qy         61 GAAACTGTGACCTGTGAGGATGCCCAAAAGACCTGCCCTGCAGTGATTGCCTGTAGCTCT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        946 GAAACTGTGACCTGTGAGGATGCCCAAAAGACCTGCCCTGCAGTGATTGCCTGTAGCTCT 1005

Qy        121 CCAGGCATCAACGGCTTCCCAGGCAAAGATGGGCGTGATGGCACCAAGGGAGAAAAGGGG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1006 CCAGGCATCAACGGCTTCCCAGGCAAAGATGGGCGTGATGGCACCAAGGGAGAAAAGGGG 1065

Qy        181 GAACCAGGCCAAGGGCTCAGAGGCTTACAGGGCCCCCCTGGAAAGTTGGGGCCTCCAGGA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1066 GAACCAGGCCAAGGGCTCAGAGGCTTACAGGGCCCCCCTGGAAAGTTGGGGCCTCCAGGA 1125

Qy        241 AATCCAGGGCCTTCTGGGTCACCAGGACCAAAGGGCCAAAAAGGAGACCCTGGAAAAAGT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1126 AATCCAGGGCCTTCTGGGTCACCAGGACCAAAGGGCCAAAAAGGAGACCCTGGAAAAAGT 1185

Qy        301 CCGGATGGTGATAGTAGCCTGGCTGCCTCAGAAAGAAAAGCTCTGCAAACAGAAATGGCA 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1186 CCGGATGGTGATAGTAGCCTGGCTGCCTCAGAAAGAAAAGCTCTGCAAACAGAAATGGCA 1245

Qy        361 CGTATCAAAAAGTGGCTGACCTTCTCTCTGGGCAAACAAGTTGGGAACAAGTTCTTCCTG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1246 CGTATCAAAAAGTGGCTGACCTTCTCTCTGGGCAAACAAGTTGGGAACAAGTTCTTCCTG 1305

Qy        421 ACCAATGGTGAAATAATGACCTTTGAAAAAGTGAAGGCCTTGTGTGTCAAGTTCCAGGCC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1306 ACCAATGGTGAAATAATGACCTTTGAAAAAGTGAAGGCCTTGTGTGTCAAGTTCCAGGCC 1365

Qy        481 TCTGTGGCCACCCCCAGGAATGCTGCAGAGAATGGAGCCATTCAGAATCTCATCAAGGAG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1366 TCTGTGGCCACCCCCAGGAATGCTGCAGAGAATGGAGCCATTCAGAATCTCATCAAGGAG 1425

Qy        541 GAAGCCTTCCTGGGCATCACTGATGAGAAGACAGAAGGGCAGTTTGTGGATCTGACAGGA 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1426 GAAGCCTTCCTGGGCATCACTGATGAGAAGACAGAAGGGCAGTTTGTGGATCTGACAGGA 1485

Qy        601 AATAGACTGACCTACACAAACTGGAACGAGGGTGAACCCAACAATGCTGGTTCTGATGAA 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1486 AATAGACTGACCTACACAAACTGGAACGAGGGTGAACCCAACAATGCTGGTTCTGATGAA 1545

Qy        661 GATTGTGTATTGCTACTGAAAAATGGCCAGTGGAATGACGTCCCCTGCTCCACCTCCCAT 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1546 GATTGTGTATTGCTACTGAAAAATGGCCAGTGGAATGACGTCCCCTGCTCCACCTCCCAT 1605

Qy        721 CTGGCCGTCTGTGAGTTCCCTATCTGA 747
              |||||||||||||||||||||||||||
Db       1606 CTGGCCGTCTGTGAGTTCCCTATCTGA 1632


RESULT 5
ADP03860
ID   ADP03860 standard; DNA; 1638 BP.
XX
AC   ADP03860;
XX
DT   29-JUL-2004  (first entry)
```

```
XX
DE   Human mbl2 DNA.
XX
KW   arteriosclerosis; severe heart disease; coronary heart disease; artery;
KW   polymorphism; human; mbl2; Chlamydia pneumoniae infection;
KW   mannose-binding lectin antigen; gene therapy; lectin-complement pathway;
KW   serine protease; ds; gene.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   variation       replace(273,g)
FT                   /*tag=  a
FT                   /standard_name= "single nucleotide polymorphism"
FT   variation       replace(602,c)
FT                   /*tag=  b
FT                   /standard_name= "single nucleotide polymorphism"
FT   CDS             821. .1638
FT                   /*tag=  c
FT                   /product= "MBL2"
FT   variation       replace(826,t)
FT                   /*tag=  d
FT                   /standard_name= "single nucleotide polymorphism"
FT   variation       replace(1045,t)
FT                   /*tag=  e
FT                   /standard_name= "single nucleotide polymorphism"
FT                   /note= "SNP results in an Arg to Cys variation"
FT   variation       replace(1052,a)
FT                   /*tag=  f
FT                   /standard_name= "single nucleotide polymorphism"
FT                   /note= "SNP results in a Gly to Asp variation"
FT   variation       replace(1061,a)
FT                   /*tag=  g
FT                   /standard_name= "single nucleotide polymorphism"
FT                   /note= "SNP results in a Gly to Glu variation"
XX
PN   DE10237393-A1.
XX
PD   11-MAR-2004.
XX
PF   12-AUG-2002; 2002DE-01037393.
XX
PR   12-AUG-2002; 2002DE-01037393.
XX
PA   (LION-) LIONEX DIAGNOSTICS & THERAPEUTICS GMBH.
XX
PI   Fuerst G,  Prohaszka Z,  Gonczol E,  Garred P,  Madsen HO;
XX
DR   WPI; 2004-258256/25.
XX
PT   Determining risk of developing arteriosclerosis or coronary artery
PT   disease, by detecting both polymorphisms in the mbl2 gene and infection
PT   by Chlamydia pneumoniae.
XX
PS   Claim 2; Fig 1; 45pp; German.
XX
CC   This invention describes a novel method for determining an indicator of
CC   the risk of developing arteriosclerosis and severe heart disease of the
CC   coronary artery type by detecting polymorphisms in the human mbl2 gene
CC   and the presence of acute, chronic or early Chlamydia pneumoniae
CC   infection. The invention comprises detecting a low concentration of the
CC   MBL (= mannose-binding lectin) antigen instead of polymorphisms in mbl2,
CC   a diagnostic kit for performing the new tests, use of at least one
CC   specific polymorphism in mbl2 for determining the risk of
CC   arteriosclerosis or severe heart disease, use of recombinant or purified
CC   human MBL for treating patients, identified by the new method, who have
CC   mlb2 polymorphisms, use of polymorphic mbl2 genes for preparation of the
CC   polymorphic isoforms of MBL protein, and use of wild-type mbl2, or its
CC   fragments, for gene therapy of subjects who have mbl2 polymorphisms. The
CC   polymorphisms are stated as being at positions -551, -221 (the promoter
CC   region), +4 (untranslated region of exon 1), +52, +54, +57 or +223 (exon
CC   1), +230 and/or +239 of the sequence deposited as Genbank Y16580.
CC   Polymorphisms are detected in genomic DNA, especially isolated from
CC   blood, by single-stranded conformational polymorphism, denaturing
CC   gradient gel electrophoresis, restriction fragment length polymorphism,
CC   sequencing or allele-specific dideoxy sequence termination and/or by
CC   ligase chain reaction. Alternatively, antibodies specific for polymorphic
CC   proteins are used. The MBL activity may be determined (in addition to, or
CC   as alternative to, measuring MBL concentration), particularly from
CC   activation of the lectin-complement pathway or from activity of serine
CC   proteases that are bound to MBL. The presence of both polymorphisms and
CC   C. pneumoniae is used to indicate a subgroup of patients with
CC   arteriosclerosis and severe heart disease of the coronary artery who are
CC   likely to benefit from treatment with antibiotics, native or recombinant
CC   MBL or vaccination against C. pneumoniae. MBL is a complement-activating
CC   protein that binds to C. pneumoniae and protects against infection. This
CC   sequence encodes the human MBL2 protein.
XX
SQ   Sequence 1638 BP; 454 A; 382 C; 430 G; 372 T; 0 U; 0 Other;

  Query Match            100.0%;  Score 747;  DB 12;  Length 1638;
  Best Local Similarity  100.0%;  Pred. No. 1.6e-207;
  Matches  747;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATGTCCCTGTTTCCATCACTCCCTCTCCTTCTCCTGAGTATGGTGGCAGCGTCTTACTCA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        892 ATGTCCCTGTTTCCATCACTCCCTCTCCTTCTCCTGAGTATGGTGGCAGCGTCTTACTCA 951

Qy         61 GAAACTGTGACCTGTGAGGATGCCCAAAAGACCTGCCCTGCAGTGATTGCCTGTAGCTCT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        952 GAAACTGTGACCTGTGAGGATGCCCAAAAGACCTGCCCTGCAGTGATTGCCTGTAGCTCT 1011

Qy        121 CCAGGCATCAACGGCTTCCCAGGCAAAGATGGGCGTGATGGCACCAAGGGAGAAAAGGGG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1012 CCAGGCATCAACGGCTTCCCAGGCAAAGATGGGCGTGATGGCACCAAGGGAGAAAAGGGG 1071

Qy        181 GAACCAGGCCAAGGGCTCAGAGGCTTACAGGGCCCCCCTGGAAAGTTGGGGCCTCCAGGA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1072 GAACCAGGCCAAGGGCTCAGAGGCTTACAGGGCCCCCCTGGAAAGTTGGGGCCTCCAGGA 1131

Qy        241 AATCCAGGGCCTTCTGGGTCACCAGGACCAAAGGGCCAAAAAGGAGACCCTGGAAAAAGT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1132 AATCCAGGGCCTTCTGGGTCACCAGGACCAAAGGGCCAAAAAGGAGACCCTGGAAAAAGT 1191

Qy        301 CCGGATGGTGATAGTAGCCTGGCTGCCTCAGAAAGAAAAGCTCTGCAAACAGAAATGGCA 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1192 CCGGATGGTGATAGTAGCCTGGCTGCCTCAGAAAGAAAAGCTCTGCAAACAGAAATGGCA 1251

Qy        361 CGTATCAAAAAGTGGCTGACCTTCTCTCTGGGCAAACAAGTTGGGAACAAGTTCTTCCTG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1252 CGTATCAAAAAGTGGCTGACCTTCTCTCTGGGCAAACAAGTTGGGAACAAGTTCTTCCTG 1311

Qy        421 ACCAATGGTGAAATAATGACCTTTGAAAAAGTGAAGGCCTTGTGTGTCAAGTTCCAGGCC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1312 ACCAATGGTGAAATAATGACCTTTGAAAAAGTGAAGGCCTTGTGTGTCAAGTTCCAGGCC 1371

Qy        481 TCTGTGGCCACCCCCAGGAATGCTGCAGAGAATGGAGCCATTCAGAATCTCATCAAGGAG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1372 TCTGTGGCCACCCCCAGGAATGCTGCAGAGAATGGAGCCATTCAGAATCTCATCAAGGAG 1431

Qy        541 GAAGCCTTCCTGGGCATCACTGATGAGAAGACAGAAGGGCAGTTTGTGGATCTGACAGGA 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1432 GAAGCCTTCCTGGGCATCACTGATGAGAAGACAGAAGGGCAGTTTGTGGATCTGACAGGA 1491

Qy        601 AATAGACTGACCTACACAAACTGGAACGAGGGTGAACCCAACAATGCTGGTTCTGATGAA 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1492 AATAGACTGACCTACACAAACTGGAACGAGGGTGAACCCAACAATGCTGGTTCTGATGAA 1551

Qy        661 GATTGTGTATTGCTACTGAAAAATGGCCAGTGGAATGACGTCCCCTGCTCCACCTCCCAT 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1552 GATTGTGTATTGCTACTGAAAAATGGCCAGTGGAATGACGTCCCCTGCTCCACCTCCCAT 1611

Qy        721 CTGGCCGTCTGTGAGTTCCCTATCTGA 747
              ||||||||||||||||||||||||||
Db       1612 CTGGCCGTCTGTGAGTTCCCTATCTGA 1638
```

```
RESULT 6
ADR29056
ID   ADR29056 standard; DNA; 1638 BP.
XX
AC   ADR29056;
XX
DT   21-OCT-2004  (first entry)
XX
DE   Human MBL gene with non-structural/variant structural allele (codon 54).
XX
KW   Sepsis; septic shock; severe; MBL; mannose binding lectin; SIRS;
KW   systemic inflammatory response syndrome; innate immune defence;
KW   single nucleotide polymorphism; SNP; structural variant; regulatory;
KW   prophylaxis; sepsis syndrome; infection susceptibility;
KW   multiple organ failure; MOF; multiple organ dysfunction; acute; gene; ds;
KW   human.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   variation       273
FT                   /*tag=  a
FT                   /standard_name= "Single nucleotide polymorphism"
FT                   /note= "Non-structural allele"
FT   variation       396
FT                   /*tag=  b
FT                   /standard_name= "Single nucleotide polymorphism"
FT                   /note= "Non-structural allele"
FT   variation       474
FT                   /*tag=  c
FT                   /standard_name= "Single nucleotide polymorphism"
FT                   /note= "Non-structural allele"
FT   variation       487
FT                   /*tag=  d
FT                   /standard_name= "Single nucleotide polymorphism"
FT                   /note= "Non-structural allele"
FT   mutation        495. .500
FT                   /*tag=  e
FT                   /note= "Optional deletion in base sequence"
FT   variation       602
FT                   /*tag=  f
FT                   /standard_name= "Single nucleotide polymorphism"
FT                   /note= "Non-structural allele"
FT   variation       753
FT                   /*tag=  g
FT                   /standard_name= "Single nucleotide polymorphism"
FT                   /note= "Non-structural allele"
FT   variation       826
FT                   /*tag=  h
FT                   /standard_name= "Single nucleotide polymorphism"
FT                   /note= "Non-structural allele"
FT   variation       1052
FT                   /*tag=  i
FT                   /standard_name= "Single nucleotide polymorphism"
FT                   /note= "Variant structural allele"
XX
PN   WO2004065626-A2.
XX
PD   05-AUG-2004.
XX
PF   16-JAN-2004; 2004WO-DK000027.
XX
PR   17-JAN-2003; 2003DK-00000042.
PR   06-MAR-2003; 2003US-0453272P.
XX
PA   (RIGS-) RIGSHOSPITALET.
PA   (KOBE-) KOBENHAVNS AMT.
XX
PI   Garred P,  Madsen HO,  Strom J;
XX
DR   WPI; 2004-571694/55.
XX
PT   Predicting whether an individual having Systemic Inflammatory Response
PT   Syndrome (SIRS) will develop sepsis, useful for treating sepsis,
PT   comprises determining the mannose-binding lectin (MBL) genotype or
PT   concentration of MBL.
XX
PS   Disclosure; SEQ ID NO 21; 65pp; English.
XX
CC   The invention relates to a method to determine the risk factor of a
CC   person for sepsis, severe sepsis or septic shock by correlating MBL
CC   (mannose binding lectin) genotype with a predefined risk value. It
CC   discloses the connection between the MBL genotype of an individual having
CC   SIRS (Systemic Inflammatory Response Syndrome) and the risk of developing
CC   sepsis, severe sepsis or septic shock. It shows how a decreased level of
CC   MBL and lack of functional MBL are crucial to the development of sepsis
CC   and septic shock in an individual having sepsis. A MBL is an important
CC   factor in innate immune defence. MBL single nucleotide polymorphism in
CC   the form of the structural variant (codon 54, codon 52 and codon 57) and
CC   regulatory variant (low expression and high expression) were studied.
CC   This invention discloses that the MBL gene polymorphism's causes a
CC   reduction of the MBL level, which is associated with the development and
CC   progression of sepsis in adult intensive care patients. The invention
CC   offers a service to determine whether an individual belongs to a risk
CC   group and it provides the treatment accordingly. There is an increased
CC   risk of a fatal outcome of an individual carrying MBL variant alleles. A
CC   rapid determination of MBL genotype of patients is important in
CC   identifying individuals at risk of developing sepsis, severe sepsis or
CC   septic shock. The MBL can be used for a medicament for the prevention and
CC   treatment of specified diseases. The MBL variant allele is also
CC   associated with an increased risk of death. It raises the prospective
CC   that MBL (MBL substitution) can be used in prophylaxis and treatment of
CC   sepsis syndrome. The frequency of MBL variant alleles is proportional to
CC   the severity of sepsis which indicates lacking buffering capacity of MBL
CC   towards initial microbial replication. It is not only associated with
CC   susceptibility of infection but also allows activation of host mechanisms
CC   central to the pathophysiology of the sepsis syndrome. The invention can
CC   also predict the risk for developing multiple organ failure (MOF),
CC   multiple organ dysfunction and acute organ dysfunction of an individual
CC   having SIRS. The high risk is characterised by the presence of at least
CC   one variant structural allele of the MBL gene and or having two low
CC   expression regulatory alleles of the MBL gene in a sample. The presented
CC   sequence is the non-structural (deletion in position 495-500) and
CC   structural allele (in codon 54) of MBL from human.
XX
SQ   Sequence 1638 BP; 454 A; 382 C; 430 G; 372 T; 0 U; 0 Other;

  Query Match             100.0%;  Score 747;  DB 13;  Length 1638;
  Best Local Similarity   100.0%;  Pred. No. 1.6e-207;
  Matches  747;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATGTCCCTGTTTCCATCACTCCCTCTCCTTCTCCTGAGTATGGTGGCAGCGTCTTACTCA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        892 ATGTCCCTGTTTCCATCACTCCCTCTCCTTCTCCTGAGTATGGTGGCAGCGTCTTACTCA 951

Qy         61 GAAACTGTGACCTGTGAGGATGCCCAAAAGACCTGCCCTGCAGTGATTGCCTGTAGCTCT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        952 GAAACTGTGACCTGTGAGGATGCCCAAAAGACCTGCCCTGCAGTGATTGCCTGTAGCTCT 1011

Qy        121 CCAGGCATCAACGGCTTCCCAGGCAAAGATGGGCGTGATGGCACCAAGGGAGAAAAGGGG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1012 CCAGGCATCAACGGCTTCCCAGGCAAAGATGGGCGTGATGGCACCAAGGGAGAAAAGGGG 1071

Qy        181 GAACCAGGCCAAGGGCTCAGAGGCTTACAGGGCCCCCCTGGAAAGTTGGGGCCTCCAGGA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1072 GAACCAGGCCAAGGGCTCAGAGGCTTACAGGGCCCCCCTGGAAAGTTGGGGCCTCCAGGA 1131

Qy        241 AATCCAGGGCCTTCTGGGTCACCAGGACCAAAGGGCCAAAAAGGAGACCCTGGAAAAAGT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1132 AATCCAGGGCCTTCTGGGTCACCAGGACCAAAGGGCCAAAAAGGAGACCCTGGAAAAAGT 1191

Qy        301 CCGGATGGTGATAGTAGCCTGGCTGCCTCAGAAAGAAAAGCTCTGCAAACAGAAATGGCA 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1192 CCGGATGGTGATAGTAGCCTGGCTGCCTCAGAAAGAAAAGCTCTGCAAACAGAAATGGCA 1251
```

```
Qy        361 CGTATCAAAAAGTGGCTGACCTTCTCTCTGGGCAAACAAGTTGGGAACAAGTTCTTCCTG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1252 CGTATCAAAAAGTGGCTGACCTTCTCTCTGGGCAAACAAGTTGGGAACAAGTTCTTCCTG 1311

Qy        421 ACCAATGGTGAAATAATGACCTTTGAAAAAGTGAAGGCCTTGTGTGTCAAGTTCCAGGCC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1312 ACCAATGGTGAAATAATGACCTTTGAAAAAGTGAAGGCCTTGTGTGTCAAGTTCCAGGCC 1371

Qy        481 TCTGTGGCCACCCCCAGGAATGCTGCAGAGAATGGAGCCATTCAGAATCTCATCAAGGAG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1372 TCTGTGGCCACCCCCAGGAATGCTGCAGAGAATGGAGCCATTCAGAATCTCATCAAGGAG 1431

Qy        541 GAAGCCTTCCTGGGCATCACTGATGAGAAGACAGAAGGGCAGTTTGTGGATCTGACAGGA 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1432 GAAGCCTTCCTGGGCATCACTGATGAGAAGACAGAAGGGCAGTTTGTGGATCTGACAGGA 1491

Qy        601 AATAGACTGACCTACACAAACTGGAACGAGGGTGAACCCAACAATGCTGGTTCTGATGAA 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1492 AATAGACTGACCTACACAAACTGGAACGAGGGTGAACCCAACAATGCTGGTTCTGATGAA 1551

Qy        661 GATTGTGTATTGCTACTGAAAAATGGCCAGTGGAATGACGTCCCCTGCTCCACCTCCCAT 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1552 GATTGTGTATTGCTACTGAAAAATGGCCAGTGGAATGACGTCCCCTGCTCCACCTCCCAT 1611

Qy        721 CTGGCCGTCTGTGAGTTCCCTATCTGA 747
              |||||||||||||||||||||||||||
Db       1612 CTGGCCGTCTGTGAGTTCCCTATCTGA 1638
```

RESULT 7
ADR29059
ID ADR29059 standard; DNA; 1638 BP.
XX
AC ADR29059;
XX
DT 21-OCT-2004 (first entry)
XX
DE Human MBL gene with high expression regulatory allele (602G).
XX
KW Sepsis; septic shock; severe; MBL; mannose binding lectin; SIRS;
KW systemic inflammatory response syndrome; innate immune defence;
KW single nucleotide polymorphism; SNP; structural variant; regulatory;
KW prophylaxis; sepsis syndrome; infection susceptibility;
KW multiple organ failure; MOF; multiple organ dysfunction; acute; gene; ds;
KW human.
XX
OS Homo sapiens.
XX

FH	Key	Location/Qualifiers
FT	variation	602
FT		/*tag= a
FT		/standard_name= "Single nucleotide polymorphism"
FT		/note= "High expression regulatory allele"
FT	variation	1045
FT		/*tag= b
FT		/standard_name= "Single nucleotide polymorphism"
FT		/note= "Normal structural allele"
FT	variation	1052
FT		/*tag= c
FT		/standard_name= "Single nucleotide polymorphism"
FT		/note= "Normal structural allele"

XX
PN WO2004065626-A2.
XX
PD 05-AUG-2004.
XX
PF 16-JAN-2004; 2004WO-DK000027.
XX
PR 17-JAN-2003; 2003DK-00000042.
PR 06-MAR-2003; 2003US-0453272P.
XX
PA (RIGS-) RIGSHOSPITALET.
PA (KOBE-) KOBENHAVNS AMT.
XX
PI Garred P, Madsen HO, Strom J;
XX
DR WPI; 2004-571694/55.
XX
PT Predicting whether an individual having Systemic Inflammatory Response
PT Syndrome (SIRS) will develop sepsis, useful for treating sepsis,
PT comprises determining the mannose-binding lectin (MBL) genotype or
PT concentration of MBL.
XX
PS Disclosure; SEQ ID NO 24; 65pp; English.
XX
CC The invention relates to a method to determine the risk factor of a
CC person for sepsis, severe sepsis or septic shock by correlating MBL
CC (mannose binding lectin) genotype with a predefined risk value. It
CC discloses the connection between the MBL genotype of an individual having
CC SIRS (Systemic Inflammatory Response Syndrome) and the risk of developing
CC sepsis, severe sepsis or septic shock. It shows how a decreased level of
CC MBL and lack of functional MBL are crucial to the development of sepsis
CC and septic shock in an individual having sepsis. A MBL is an important
CC factor in innate immune defence. MBL single nucleotide polymorphism in
CC the form of the structural variant (codon 54, codon 52 and codon 57) and
CC regulatory variant (low expression and high expression) were studied.
CC This invention discloses that the MBL gene polymorphism's causes a
CC reduction of the MBL level, which is associated with the development and
CC progression of sepsis in adult intensive care patients. The invention
CC offers a service to determine whether an individual belongs to a risk
CC group and it provides the treatment accordingly. There is an increased
CC risk of a fatal outcome of an individual carrying MBL variant alleles. A
CC rapid determination of MBL genotype of patients is important in
CC identifying individuals at risk of developing sepsis, severe sepsis or
CC septic shock. The MBL can be used for a medicament for the prevention and
CC treatment of specified diseases. The MBL variant allele is also
CC associated with an increased risk of death. It raises the prospective
CC that MBL (MBL substitution) can be used in prophylaxis and treatment of
CC sepsis syndrome. The frequency of MBL variant alleles is proportional to
CC the severity of sepsis which indicates lacking buffering capacity of MBL
CC towards initial microbial replication. It is not only associated with
CC susceptibility of infection but also allows activation of host mechanisms
CC central to the pathophysiology of the sepsis syndrome. The invention can
CC also predict the risk for developing multiple organ failure (MOF),
CC multiple organ dysfunction and acute organ dysfunction of an individual
CC having SIRS. The high risk is characterised by the presence of at least
CC one variant structural allele of the MBL gene and or having two low
CC expression regulatory alleles of the MBL gene in a sample. The presented
CC sequence is the high expression regulatory allele (position 602 has a
CC base G substitution) of MBL (mannose binding lectin) gene from human.
XX
SQ Sequence 1638 BP; 454 A; 381 C; 431 G; 372 T; 0 U; 0 Other;

Query Match 100.0%; Score 747; DB 13; Length 1638;
Best Local Similarity 100.0%; Pred. No. 1.6e-207;
Matches 747; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 ATGTCCCTGTTTCCATCACTCCCTCTCCTTCTCCTGAGTATGGTGGCAGCGTCTTACTCA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        892 ATGTCCCTGTTTCCATCACTCCCTCTCCTTCTCCTGAGTATGGTGGCAGCGTCTTACTCA 951

Qy         61 GAAACTGTGACCTGTGAGGATGCCCAAAAGACCTGCCCTGCAGTGATTGCCTGTAGCTCT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        952 GAAACTGTGACCTGTGAGGATGCCCAAAAGACCTGCCCTGCAGTGATTGCCTGTAGCTCT 1011

Qy        121 CCAGGCATCAACGGCTTCCCAGGCAAAGATGGGCGTGATGGCACCAAGGGAGAAAAGGGG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1012 CCAGGCATCAACGGCTTCCCAGGCAAAGATGGGCGTGATGGCACCAAGGGAGAAAAGGGG 1071

Qy        181 GAACCAGGCCAAGGGCTCAGAGGCTTACAGGGCCCCCCTGGAAAGTTGGGGCCTCCAGGA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1072 GAACCAGGCCAAGGGCTCAGAGGCTTACAGGGCCCCCCTGGAAAGTTGGGGCCTCCAGGA 1131

Qy        241 AATCCAGGGCCTTCTGGGTCACCAGGACCAAAGGGCCAAAAAGGAGACCCTGGAAAAAGT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1132 AATCCAGGGCCTTCTGGGTCACCAGGACCAAAGGGCCAAAAAGGAGACCCTGGAAAAAGT 1191
```

```
Qy       301 CCGGATGGTGATAGTAGCCTGGCTGCCTCAGAAAGAAAAGCTCTGCAAACAGAAATGGCA 360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1192 CCGGATGGTGATAGTAGCCTGGCTGCCTCAGAAAGAAAAGCTCTGCAAACAGAAATGGCA 1251

Qy       361 CGTATCAAAAAGTGGCTGACCTTCTCTCTCTGGGCAAACAAGTTGGGAACAAGTTCTTCCTG 420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1252 CGTATCAAAAAGTGGCTGACCTTCTCTCTCTGGGCAAACAAGTTGGGAACAAGTTCTTCCTG 1311

Qy       421 ACCAATGGTGAAATAATGACCTTTGAAAAAGTGAAGGCCTTGTGTGTCAAGTTCCAGGCC 480
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1312 ACCAATGGTGAAATAATGACCTTTGAAAAAGTGAAGGCCTTGTGTGTCAAGTTCCAGGCC 1371

Qy       481 TCTGTGGCCACCCCCAGGAATGCTGCAGAGAATGGAGCCATTCAGAATCTCATCAAGGAG 540
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1372 TCTGTGGCCACCCCCAGGAATGCTGCAGAGAATGGAGCCATTCAGAATCTCATCAAGGAG 1431

Qy       541 GAAGCCTTCCTGGGCATCACTGATGAGAAGACAGAAGGGCAGTTTGTGGATCTGACAGGA 600
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1432 GAAGCCTTCCTGGGCATCACTGATGAGAAGACAGAAGGGCAGTTTGTGGATCTGACAGGA 1491

Qy       601 AATAGACTGACCTACACAAACTGGAACGAGGGTGAACCCAACAATGCTGGTTCTGATGAA 660
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1492 AATAGACTGACCTACACAAACTGGAACGAGGGTGAACCCAACAATGCTGGTTCTGATGAA 1551

Qy       661 GATTGTGTATTGCTACTGAAAAATGGCCAGTGGAATGACGTCCCCTGCTCCACCTCCCAT 720
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1552 GATTGTGTATTGCTACTGAAAAATGGCCAGTGGAATGACGTCCCCTGCTCCACCTCCCAT 1611

Qy       721 CTGGCCGTCTGTGAGTTCCCTATCTGA 747
            ||||||||||||||||||||||||||
Db      1612 CTGGCCGTCTGTGAGTTCCCTATCTGA 1638
```

RESULT 8
ADR29061
ID ADR29061 standard; DNA; 1638 BP.
XX
AC ADR29061;
XX
DT 21-OCT-2004 (first entry)
XX
DE Human MBL low expression regulatory allele (position 602).
XX
KW Sepsis; septic shock; severe; MBL; mannose binding lectin; SIRS;
KW systemic inflammatory response syndrome; innate immune defence;
KW single nucleotide polymorphism; SNP; structural variant; regulatory;
KW prophylaxis; sepsis syndrome; infection susceptibility;
KW multiple organ failure; MOF; multiple organ dysfunction; acute; gene; ds;
KW human.
XX
OS Homo sapiens.
XX

FH	Key	Location/Qualifiers
FT	variation	602
FT		/*tag= a
FT		/standard_name= "Single nucleotide polymorphism"
FT		/note= "Low expression regulatory allele"

XX
PN WO2004065626-A2.
XX
PD 05-AUG-2004.
XX
PF 16-JAN-2004; 2004WO-DK000027.
XX
PR 17-JAN-2003; 2003DK-00000042.
PR 06-MAR-2003; 2003US-0453272P.
XX
PA (RIGS-) RIGSHOSPITALET.
PA (KOBE-) KOBENHAVNS AMT.
XX
PI Garred P, Madsen HO, Strom J;
XX
DR WPI; 2004-571694/55.
XX
PT Predicting whether an individual having Systemic Inflammatory Response
PT Syndrome (SIRS) will develop sepsis, useful for treating sepsis,
PT comprises determining the mannose-binding lectin (MBL) genotype or
PT concentration of MBL.
XX
PS Claim 5; SEQ ID NO 26; 65pp; English.
XX
CC The invention relates to a method to determine the risk factor of a
CC person for sepsis, severe sepsis or septic shock by correlating MBL
CC (mannose binding lectin) genotype with a predefined risk value. It
CC discloses the connection between the MBL genotype of an individual having
CC SIRS (Systemic Inflammatory Response Syndrome) and the risk of developing
CC sepsis, severe sepsis or septic shock. It shows how a decreased level of
CC MBL and lack of functional MBL are crucial to the development of sepsis
CC and septic shock in an individual having sepsis. A MBL is an important
CC factor in innate immune defence. MBL single nucleotide polymorphism in
CC the form of the structural variant (codon 54, codon 52 and codon 57) and
CC regulatory variant (low expression and high expression) were studied.
CC This invention discloses that the MBL gene polymorphism's causes a
CC reduction of the MBL level, which is associated with the development and
CC progression of sepsis in adult intensive care patients. The invention
CC offers a service to determine whether an individual belongs to a risk
CC group and it provides the treatment accordingly. There is an increased
CC risk of a fatal outcome of an individual carrying MBL variant alleles. A
CC rapid determination of MBL genotype of patients is important in
CC identifying individuals at risk of developing sepsis, severe sepsis or
CC septic shock. The MBL can be used for a medicament for the prevention and
CC treatment of specified diseases. The MBL variant allele is also
CC associated with an increased risk of death. It raises the prospective
CC that MBL (MBL substitution) can be used in prophylaxis and treatment of
CC sepsis syndrome. The frequency of MBL variant alleles is proportional to
CC the severity of sepsis which indicates lacking buffering capacity of MBL
CC towards initial microbial replication. It is not only associated with
CC susceptibility of infection but also allows activation of host mechanisms
CC central to the pathophysiology of the sepsis syndrome. The invention can
CC also predict the risk for developing multiple organ failure (MOF),
CC multiple organ dysfunction and acute organ dysfunction of an individual
CC having SIRS. The high risk is characterised by the presence of at least
CC one variant structural allele of the MBL gene and or having two low
CC expression regulatory alleles of the MBL gene in a sample. The presented
CC sequence is the low expression regulatory allele (position 602 has a base
CC C substitution) of MBL (mannose binding lectin) gene from human.
XX
SQ Sequence 1638 BP; 454 A; 383 C; 429 G; 372 T; 0 U; 0 Other;

Query Match 100.0%; Score 747; DB 13; Length 1638;
Best Local Similarity 100.0%; Pred. No. 1.6e-207;
Matches 747; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy         1 ATGTCCCTGTTTCCATCACTCCCTCTCCTTCTCCTGAGTATGGTGGCAGCGTCTTACTCA 60
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       892 ATGTCCCTGTTTCCATCACTCCCTCTCCTTCTCCTGAGTATGGTGGCAGCGTCTTACTCA 951

Qy        61 GAAACTGTGACCTGTGAGGATGCCCAAAAGACCTGCCCTGCAGTGATTGCCTGTAGCTCT 120
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       952 GAAACTGTGACCTGTGAGGATGCCCAAAAGACCTGCCCTGCAGTGATTGCCTGTAGCTCT 1011

Qy       121 CCAGGCATCAACGGCTTCCCAGGCAAAGATGGGCGTGATGGCACCAAGGGAGAAAAGGGG 180
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1012 CCAGGCATCAACGGCTTCCCAGGCAAAGATGGGCGTGATGGCACCAAGGGAGAAAAGGGG 1071

Qy       181 GAACCAGGCCAAGGGCTCAGAGGCTTACAGGGCCCCCCTGGAAAGTTGGGGCCTCCAGGA 240
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1072 GAACCAGGCCAAGGGCTCAGAGGCTTACAGGGCCCCCCTGGAAAGTTGGGGCCTCCAGGA 1131

Qy       241 AATCCAGGGCCTTCTGGGTCACCAGGACCAAAGGGCCAAAAAGGAGACCCTGGAAAAAGT 300
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1132 AATCCAGGGCCTTCTGGGTCACCAGGACCAAAGGGCCAAAAAGGAGACCCTGGAAAAAGT 1191

Qy       301 CCGGATGGTGATAGTAGCCTGGCTGCCTCAGAAAGAAAAGCTCTGCAAACAGAAATGGCA 360
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

```
Db       1192 CCGGATGGTGATAGTAGCCTGGCTGCCTCAGAAAGAAAAGCTCTGCAAACAGAAATGGCA 1251

Qy        361 CGTATCAAAAAGTGGCTGACCTTCTCTCTGGGCAAACAAGTTGGGAACAAGTTCTTCCTG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1252 CGTATCAAAAAGTGGCTGACCTTCTCTCTGGGCAAACAAGTTGGGAACAAGTTCTTCCTG 1311

Qy        421 ACCAATGGTGAAATAATGACCTTTGAAAAAGTGAAGGCCTTGTGTGTCAAGTTCCAGGCC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1312 ACCAATGGTGAAATAATGACCTTTGAAAAAGTGAAGGCCTTGTGTGTCAAGTTCCAGGCC 1371

Qy        481 TCTGTGGCCACCCCCAGGAATGCTGCAGAGAATGGAGCCATTCAGAATCTCATCAAGGAG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1372 TCTGTGGCCACCCCCAGGAATGCTGCAGAGAATGGAGCCATTCAGAATCTCATCAAGGAG 1431

Qy        541 GAAGCCTTCCTGGGCATCACTGATGAGAAGACAGAAGGGCAGTTTGTGGATCTGACAGGA 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1432 GAAGCCTTCCTGGGCATCACTGATGAGAAGACAGAAGGGCAGTTTGTGGATCTGACAGGA 1491

Qy        601 AATAGACTGACCTACACAAACTGGAACGAGGGTGAACCCAACAATGCTGGTTCTGATGAA 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1492 AATAGACTGACCTACACAAACTGGAACGAGGGTGAACCCAACAATGCTGGTTCTGATGAA 1551

Qy        661 GATTGTGTATTGCTACTGAAAAATGGCCAGTGGAATGACGTCCCCTGCTCCACCTCCCAT 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1552 GATTGTGTATTGCTACTGAAAAATGGCCAGTGGAATGACGTCCCCTGCTCCACCTCCCAT 1611

Qy        721 CTGGCCGTCTGTGAGTTCCCTATCTGA 747
              |||||||||||||||||||||||||||
Db       1612 CTGGCCGTCTGTGAGTTCCCTATCTGA 1638
```

RESULT 9
AAZ07143
ID AAZ07143 standard; cDNA; 3605 BP.
XX
AC AAZ07143;
XX
DT 11-OCT-1999 (first entry)
XX
DE Human mannan-binding protein encoding cDNA.
XX
KW Human; mannan-binding protein; hMBP; recombinant; inhibition; infection;
KW rhMBP; haemagglutination; influenza; HIV; primer; ss.
XX
OS Homo sapiens.
XX

FH	Key	Location/Qualifiers
FT	CDS	66. .812
FT		/*tag= a
FT	sig_peptide	66. .125
FT		/*tag= b
FT	mat_peptide	126. .809
FT		/*tag= c
FT		/product= "mannan-binding protein"

XX
PN WO9937676-A1.
XX
PD 29-JUL-1999.
XX
PF 23-JUL-1998; 98WO-JP003311.
XX
PR 23-JAN-1998; 98JP-00011864.
XX
PA (FUSO) FUSO PHARM IND LTD.
XX
PI Wakamiya N;
XX
DR WPI; 1999-469114/39.
DR P-PSDB; AAY29485.
XX
PT Recombinant human mannan-binding protein expressed using pNOW1 vector.
XX
PS Disclosure; Page 71-74; 91pp; Japanese.
XX
CC The present invention describes recombinant human mannan-binding protein
CC (rhMBP) having a molecular weight range of 1000-1300 or 200-400 kDa (by
CC gel filtration with detection at 280 nm). rhMBP may be used as a
CC component of drug compositions for the inhibition of haemagglutination
CC and prevention of infection by viruses such as influenza and HIV. The
CC present sequence encodes hMBP (human mannan-binding protein)
XX
SQ Sequence 3605 BP; 1055 A; 679 C; 647 G; 1224 T; 0 U; 0 Other;

Query Match 100.0%; Score 747; DB 2; Length 3605;
Best Local Similarity 100.0%; Pred. No. 2.3e-207;
Matches 747; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 ATGTCCCTGTTTCCATCACTCCCTCTCCTTCTCCTGAGTATGGTGGCAGCGTCTTACTCA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         66 ATGTCCCTGTTTCCATCACTCCCTCTCCTTCTCCTGAGTATGGTGGCAGCGTCTTACTCA 125

Qy         61 GAAACTGTGACCTGTGAGGATGCCCAAAAGACCTGCCCTGCAGTGATTGCCTGTAGCTCT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        126 GAAACTGTGACCTGTGAGGATGCCCAAAAGACCTGCCCTGCAGTGATTGCCTGTAGCTCT 185

Qy        121 CCAGGCATCAACGGCTTCCCAGGCAAAGATGGGCGTGATGGCACCAAGGGAGAAAAGGGG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        186 CCAGGCATCAACGGCTTCCCAGGCAAAGATGGGCGTGATGGCACCAAGGGAGAAAAGGGG 245

Qy        181 GAACCAGGCCAAGGGCTCAGAGGCTTACAGGGCCCCCCTGGAAAGTTGGGGCCTCCAGGA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        246 GAACCAGGCCAAGGGCTCAGAGGCTTACAGGGCCCCCCTGGAAAGTTGGGGCCTCCAGGA 305

Qy        241 AATCCAGGGCCTTCTGGGTCACCAGGACCAAAGGGCCAAAAAGGAGACCCTGGAAAAAGT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        306 AATCCAGGGCCTTCTGGGTCACCAGGACCAAAGGGCCAAAAAGGAGACCCTGGAAAAAGT 365

Qy        301 CCGGATGGTGATAGTAGCCTGGCTGCCTCAGAAAGAAAAGCTCTGCAAACAGAAATGGCA 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        366 CCGGATGGTGATAGTAGCCTGGCTGCCTCAGAAAGAAAAGCTCTGCAAACAGAAATGGCA 425

Qy        361 CGTATCAAAAAGTGGCTGACCTTCTCTCTGGGCAAACAAGTTGGGAACAAGTTCTTCCTG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        426 CGTATCAAAAAGTGGCTGACCTTCTCTCTGGGCAAACAAGTTGGGAACAAGTTCTTCCTG 485

Qy        421 ACCAATGGTGAAATAATGACCTTTGAAAAAGTGAAGGCCTTGTGTGTCAAGTTCCAGGCC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        486 ACCAATGGTGAAATAATGACCTTTGAAAAAGTGAAGGCCTTGTGTGTCAAGTTCCAGGCC 545

Qy        481 TCTGTGGCCACCCCCAGGAATGCTGCAGAGAATGGAGCCATTCAGAATCTCATCAAGGAG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        546 TCTGTGGCCACCCCCAGGAATGCTGCAGAGAATGGAGCCATTCAGAATCTCATCAAGGAG 605

Qy        541 GAAGCCTTCCTGGGCATCACTGATGAGAAGACAGAAGGGCAGTTTGTGGATCTGACAGGA 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        606 GAAGCCTTCCTGGGCATCACTGATGAGAAGACAGAAGGGCAGTTTGTGGATCTGACAGGA 665

Qy        601 AATAGACTGACCTACACAAACTGGAACGAGGGTGAACCCAACAATGCTGGTTCTGATGAA 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        666 AATAGACTGACCTACACAAACTGGAACGAGGGTGAACCCAACAATGCTGGTTCTGATGAA 725

Qy        661 GATTGTGTATTGCTACTGAAAAATGGCCAGTGGAATGACGTCCCCTGCTCCACCTCCCAT 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        726 GATTGTGTATTGCTACTGAAAAATGGCCAGTGGAATGACGTCCCCTGCTCCACCTCCCAT 785

Qy        721 CTGGCCGTCTGTGAGTTCCCTATCTGA 747
              |||||||||||||||||||||||||||
Db        786 CTGGCCGTCTGTGAGTTCCCTATCTGA 812
```

RESULT 10
ABN97210
ID ABN97210 standard; DNA; 3605 BP.
XX
AC ABN97210;
XX

DT 13-AUG-2002 (first entry)
XX
DE Gene #3708 used to diagnose liver cancer.
XX
KW Gene; liver cancer; ds; hepatocellular carcinoma; hepatotropic;
KW metastatic liver tumour; cytostatic; expression profile; disease state;
KW disease progression; drug toxicity; drug efficacy; drug metabolism.
XX
OS Homo sapiens.
XX
PN WO200229103-A2.
XX
PD 11-APR-2002.
XX
PF 02-OCT-2001; 2001WO-US030589.
XX
PR 02-OCT-2000; 2000US-0237054P.
XX
PA (GENE-) GENE LOGIC INC.
XX
PI Horne D, Alvares C, Peres-Da-Silva S, Vockley JG;
XX
DR WPI; 2002-426119/45.
XX
PT Diagnosing and detecting the progression of liver cancer, hepatocellular
PT carcinoma or metastatic liver tumor in a patient, involves detecting the
PT level of expression of two or more genes in a liver tissue sample.
XX
PS Claim 1; SEQ ID NO 3708; 298pp; English.
XX
CC The invention relates to a novel method for diagnosing and detecting the
CC progression of liver cancer, hepatocellular carcinoma or metastatic liver
CC tumour in a patient, and differentiating metastatic liver cancer from
CC hepatocellular carcinoma in a patient, involving detecting the level of
CC expression of two or more genes represented in ABN93503-ABN97455 in a
CC tissue sample. The method of the invention has hepatotropic, and
CC cytostatic activity. The method is useful for diagnosing and detecting
CC the progression of liver cancer, hepatocellular carcinoma and metastatic
CC liver carcinoma in a patient. The method is useful for identifying
CC expression profiles which serve as useful diagnostic markers as well as
CC markers that can be used to monitor disease states, disease progression,
CC drug toxicity, drug efficacy and drug metabolism. Note: The sequence data
CC for this patent did not form part of the printed specification, but was
CC obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 3605 BP; 1055 A; 679 C; 647 G; 1224 T; 0 U; 0 Other;

Query Match 100.0%; Score 747; DB 6; Length 3605;
Best Local Similarity 100.0%; Pred. No. 2.3e-207;
Matches 747; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 ATGTCCCTGTTTCCATCACTCCCTCTCCTTCTCCTGAGTATGGTGGCAGCGTCTTACTCA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         66 ATGTCCCTGTTTCCATCACTCCCTCTCCTTCTCCTGAGTATGGTGGCAGCGTCTTACTCA 125

Qy         61 GAAACTGTGACCTGTGAGGATGCCCAAAAGACCTGCCCTGCAGTGATTGCCTGTAGCTCT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        126 GAAACTGTGACCTGTGAGGATGCCCAAAAGACCTGCCCTGCAGTGATTGCCTGTAGCTCT 185

Qy        121 CCAGGCATCAACGGCTTCCCAGGCAAAGATGGGCGTGATGGCACCAAGGGAGAAAAGGGG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        186 CCAGGCATCAACGGCTTCCCAGGCAAAGATGGGCGTGATGGCACCAAGGGAGAAAAGGGG 245

Qy        181 GAACCAGGCCAAGGGCTCAGAGGCTTACAGGGCCCCCCTGGAAAGTTGGGGCCTCCAGGA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        246 GAACCAGGCCAAGGGCTCAGAGGCTTACAGGGCCCCCCTGGAAAGTTGGGGCCTCCAGGA 305

Qy        241 AATCCAGGGCCTTCTGGGTCACCAGGACCAAAGGGCCAAAAAGGAGACCCTGGAAAAAGT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        306 AATCCAGGGCCTTCTGGGTCACCAGGACCAAAGGGCCAAAAAGGAGACCCTGGAAAAAGT 365

Qy        301 CCGGATGGTGATAGTAGCCTGGCTGCCTCAGAAAGAAAAGCTCTGCAAACAGAAATGGCA 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        366 CCGGATGGTGATAGTAGCCTGGCTGCCTCAGAAAGAAAAGCTCTGCAAACAGAAATGGCA 425

Qy        361 CGTATCAAAAAGTGGCTGACCTTCTCTCTGGGCAAACAAGTTGGGAACAAGTTCTTCCTG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        426 CGTATCAAAAAGTGGCTGACCTTCTCTCTGGGCAAACAAGTTGGGAACAAGTTCTTCCTG 485

Qy        421 ACCAATGGTGAAATAATGACCTTTGAAAAAGTGAAGGCCTTGTGTGTCAAGTTCCAGGCC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        486 ACCAATGGTGAAATAATGACCTTTGAAAAAGTGAAGGCCTTGTGTGTCAAGTTCCAGGCC 545

Qy        481 TCTGTGGCCACCCCCAGGAATGCTGCAGAGAATGGAGCCATTCAGAATCTCATCAAGGAG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        546 TCTGTGGCCACCCCCAGGAATGCTGCAGAGAATGGAGCCATTCAGAATCTCATCAAGGAG 605

Qy        541 GAAGCCTTCCTGGGCATCACTGATGAGAAGACAGAAGGGCAGTTTGTGGATCTGACAGGA 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        606 GAAGCCTTCCTGGGCATCACTGATGAGAAGACAGAAGGGCAGTTTGTGGATCTGACAGGA 665

Qy        601 AATAGACTGACCTACACAAACTGGAACGAGGGTGAACCCAACAATGCTGGTTCTGATGAA 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        666 AATAGACTGACCTACACAAACTGGAACGAGGGTGAACCCAACAATGCTGGTTCTGATGAA 725

Qy        661 GATTGTGTATTGCTACTGAAAAATGGCCAGTGGAATGACGTCCCCTGCTCCACCTCCCAT 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        726 GATTGTGTATTGCTACTGAAAAATGGCCAGTGGAATGACGTCCCCTGCTCCACCTCCCAT 785

Qy        721 CTGGCCGTCTGTGAGTTCCCTATCTGA 747
              |||||||||||||||||||||||||||
Db        786 CTGGCCGTCTGTGAGTTCCCTATCTGA 812
```

RESULT 11
ADI20099
ID ADI20099 standard; DNA; 3605 BP.
XX
AC ADI20099;
XX
DT 22-APR-2004 (first entry)
XX
DE DNA sequence #1 related to the invention.
XX
KW anti-human immunodeficiency virus; HIV; mannose binding protein; MBP; ds.
XX
OS Homo sapiens.
XX
PN WO2004002511-A1.
XX
PD 08-JAN-2004.
XX
PF 30-JUN-2003; 2003WO-JP008259.
XX
PR 28-JUN-2002; 2002JP-00189534.
XX
PA (FUSO) FUSO PHARM IND LTD.
XX
PI Wakamiya N, Ohtani K, Sakamoto T, Keshi H, Kishi Y;
XX
DR WPI; 2004-082879/08.
XX
PT Anti-human immunodeficiency virus (HIV) agent comprising a mannose
PT binding protein for treatment of HIV infection.
XX
PS Disclosure; SEQ ID NO 1; 44pp; Japanese.
XX
CC The present invention relates to anti-human immunodeficiency virus (HIV)
CC agent comprises a mannose binding protein (MBP). For use in the treatment
CC of HIV. The present sequence represents a DNA sequence related to the
CC invention.
XX
SQ Sequence 3605 BP; 1055 A; 679 C; 647 G; 1224 T; 0 U; 0 Other;

Query Match 100.0%; Score 747; DB 12; Length 3605;

```
  Best Local Similarity   100.0%;  Pred. No. 2.3e-207;
  Matches  747;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATGTCCCTGTTTCCATCACTCCCTCTCCTTCTCCTGAGTATGGTGGCAGCGTCTTACTCA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         66 ATGTCCCTGTTTCCATCACTCCCTCTCCTTCTCCTGAGTATGGTGGCAGCGTCTTACTCA 125

Qy         61 GAAACTGTGACCTGTGAGGATGCCCAAAAGACCTGCCCTGCAGTGATTGCCTGTAGCTCT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        126 GAAACTGTGACCTGTGAGGATGCCCAAAAGACCTGCCCTGCAGTGATTGCCTGTAGCTCT 185

Qy        121 CCAGGCATCAACGGCTTCCCAGGCAAAGATGGGCGTGATGGCACCAAGGGAGAAAAGGGG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        186 CCAGGCATCAACGGCTTCCCAGGCAAAGATGGGCGTGATGGCACCAAGGGAGAAAAGGGG 245

Qy        181 GAACCAGGCCAAGGGCTCAGAGGCTTACAGGGCCCCCCTGGAAAGTTGGGGCCTCCAGGA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        246 GAACCAGGCCAAGGGCTCAGAGGCTTACAGGGCCCCCCTGGAAAGTTGGGGCCTCCAGGA 305

Qy        241 AATCCAGGGCCTTCTGGGTCACCAGGACCAAAGGGCCAAAAAGGAGACCCTGGAAAAAGT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        306 AATCCAGGGCCTTCTGGGTCACCAGGACCAAAGGGCCAAAAAGGAGACCCTGGAAAAAGT 365

Qy        301 CCGGATGGTGATAGTAGCCTGGCTGCCTCAGAAAGAAAAGCTCTGCAAACAGAAATGGCA 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        366 CCGGATGGTGATAGTAGCCTGGCTGCCTCAGAAAGAAAAGCTCTGCAAACAGAAATGGCA 425

Qy        361 CGTATCAAAAAGTGGCTGACCTTCTCTCTGGGCAAACAAGTTGGGAACAAGTTCTTCCTG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        426 CGTATCAAAAAGTGGCTGACCTTCTCTCTGGGCAAACAAGTTGGGAACAAGTTCTTCCTG 485

Qy        421 ACCAATGGTGAAATAATGACCTTTGAAAAAGTGAAGGCCTTGTGTGTCAAGTTCCAGGCC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        486 ACCAATGGTGAAATAATGACCTTTGAAAAAGTGAAGGCCTTGTGTGTCAAGTTCCAGGCC 545

Qy        481 TCTGTGGCCACCCCCAGGAATGCTGCAGAGAATGGAGCCATTCAGAATCTCATCAAGGAG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        546 TCTGTGGCCACCCCCAGGAATGCTGCAGAGAATGGAGCCATTCAGAATCTCATCAAGGAG 605

Qy        541 GAAGCCTTCCTGGGCATCACTGATGAGAAGACAGAAGGGCAGTTTGTGGATCTGACAGGA 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        606 GAAGCCTTCCTGGGCATCACTGATGAGAAGACAGAAGGGCAGTTTGTGGATCTGACAGGA 665

Qy        601 AATAGACTGACCTACACAAACTGGAACGAGGGTGAACCCAACAATGCTGGTTCTGATGAA 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        666 AATAGACTGACCTACACAAACTGGAACGAGGGTGAACCCAACAATGCTGGTTCTGATGAA 725

Qy        661 GATTGTGTATTGCTACTGAAAAATGGCCAGTGGAATGACGTCCCCTGCTCCACCTCCCAT 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        726 GATTGTGTATTGCTACTGAAAAATGGCCAGTGGAATGACGTCCCCTGCTCCACCTCCCAT 785

Qy        721 CTGGCCGTCTGTGAGTTCCCTATCTGA 747
              |||||||||||||||||||||||||||
Db        786 CTGGCCGTCTGTGAGTTCCCTATCTGA 812


RESULT 12
ADJ45526
ID   ADJ45526 standard; cDNA; 3605 BP.
XX
AC   ADJ45526;
XX
DT   06-MAY-2004  (first entry)
XX
DE   cDNA encoding LXR-ligand induced transcript seq id 57.
XX
KW   LXR; liver X receptor; cholesterol; gallstone; atherosclerosis;
KW   lipid storage disease; obesity; diabetes; hypercholesterolaemia;
KW   LXR-ligand induced 1; LXRLI1; human; LXR-ligand induced transcript;
KW   LXR regulated gene; ss; gene.
XX
OS   Homo sapiens.
XX
PN   US2004023276-A1.
XX
PD   05-FEB-2004.
XX
PF   02-MAY-2003; 2003US-00429160.
XX
PR   03-MAY-2002; 2002US-0377714P.
XX
PA   (WARD/) WARD T R.
PA   (MAOM/) MAO M.
PA   (LINS/) LINSLEY P S.
PA   (LUND/) LUND E.
XX
PI   Ward TR,  Mao M,  Linsley PS,  Lund E;
XX
DR   WPI; 2004-224687/21.
DR   P-PSDB; ADJ45527.
XX
PT   New purified Liver X receptor (LXR) nucleic acids, useful for diagnosing
PT   a disease involving LXR activity, such as cholesterol gallstones,
PT   atherosclerosis, lipid storage diseases, obesity, diabetes, or
PT   hypercholesterolemia.
XX
PS   Example 1; SEQ ID NO 57; 141pp; English.
XX
CC   The invention describes a purified nucleic acid comprising a fully
CC   defined sequence of 1586 bp (SEQ ID NO: 1) as given in the specification,
CC   or its complement. The methods and compositions are useful for diagnosing
CC   a disease or disorder involving LXR (liver X receptor) activity in a
CC   sample by detecting an increase or decrease in the transcript level
CC   relative to the amount present in an analogous sample from a subject not
CC   having the disease or disorder or not subjected to therapy, wherein the
CC   disease or disorder is cholesterol gallstones, atherosclerosis, lipid
CC   storage diseases, obesity, diabetes, or hypercholesterolaemia. They are
CC   also used to identify a compound that changes LXR activity, wherein the
CC   compound changes the estimated level of LXR activity in a sample from the
CC   subject contacted with the compound relative to the estimated level of
CC   LXR activity in an analogous sample from the subject not contacted with
CC   the compound. This sequence encodes an LXR regulated protein.
XX
SQ   Sequence 3605 BP; 1055 A; 679 C; 647 G; 1224 T; 0 U; 0 Other;

  Query Match           100.0%;  Score 747;  DB 12;  Length 3605;
  Best Local Similarity   100.0%;  Pred. No. 2.3e-207;
  Matches  747;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATGTCCCTGTTTCCATCACTCCCTCTCCTTCTCCTGAGTATGGTGGCAGCGTCTTACTCA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         66 ATGTCCCTGTTTCCATCACTCCCTCTCCTTCTCCTGAGTATGGTGGCAGCGTCTTACTCA 125

Qy         61 GAAACTGTGACCTGTGAGGATGCCCAAAAGACCTGCCCTGCAGTGATTGCCTGTAGCTCT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        126 GAAACTGTGACCTGTGAGGATGCCCAAAAGACCTGCCCTGCAGTGATTGCCTGTAGCTCT 185

Qy        121 CCAGGCATCAACGGCTTCCCAGGCAAAGATGGGCGTGATGGCACCAAGGGAGAAAAGGGG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        186 CCAGGCATCAACGGCTTCCCAGGCAAAGATGGGCGTGATGGCACCAAGGGAGAAAAGGGG 245

Qy        181 GAACCAGGCCAAGGGCTCAGAGGCTTACAGGGCCCCCCTGGAAAGTTGGGGCCTCCAGGA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        246 GAACCAGGCCAAGGGCTCAGAGGCTTACAGGGCCCCCCTGGAAAGTTGGGGCCTCCAGGA 305

Qy        241 AATCCAGGGCCTTCTGGGTCACCAGGACCAAAGGGCCAAAAAGGAGACCCTGGAAAAAGT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        306 AATCCAGGGCCTTCTGGGTCACCAGGACCAAAGGGCCAAAAAGGAGACCCTGGAAAAAGT 365

Qy        301 CCGGATGGTGATAGTAGCCTGGCTGCCTCAGAAAGAAAAGCTCTGCAAACAGAAATGGCA 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        366 CCGGATGGTGATAGTAGCCTGGCTGCCTCAGAAAGAAAAGCTCTGCAAACAGAAATGGCA 425

Qy        361 CGTATCAAAAAGTGGCTGACCTTCTCTCTGGGCAAACAAGTTGGGAACAAGTTCTTCCTG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        426 CGTATCAAAAAGTGGCTGACCTTCTCTCTGGGCAAACAAGTTGGGAACAAGTTCTTCCTG 485
```

```
Qy        421 ACCAATGGTGAAATAATGACCTTTGAAAAAGTGAAGGCCTTGTGTGTCAAGTTCCAGGCC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        486 ACCAATGGTGAAATAATGACCTTTGAAAAAGTGAAGGCCTTGTGTGTCAAGTTCCAGGCC 545

Qy        481 TCTGTGGCCACCCCCAGGAATGCTGCAGAGAATGGAGCCATTCAGAATCTCATCAAGGAG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        546 TCTGTGGCCACCCCCAGGAATGCTGCAGAGAATGGAGCCATTCAGAATCTCATCAAGGAG 605

Qy        541 GAAGCCTTCCTGGGCATCACTGATGAGAAGACAGAAGGGCAGTTTGTGGATCTGACAGGA 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        606 GAAGCCTTCCTGGGCATCACTGATGAGAAGACAGAAGGGCAGTTTGTGGATCTGACAGGA 665

Qy        601 AATAGACTGACCTACACAAACTGGAACGAGGGTGAACCCAACAATGCTGGTTCTGATGAA 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        666 AATAGACTGACCTACACAAACTGGAACGAGGGTGAACCCAACAATGCTGGTTCTGATGAA 725

Qy        661 GATTGTGTATTGCTACTGAAAAATGGCCAGTGGAATGACGTCCCCTGCTCCACCTCCCAT 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        726 GATTGTGTATTGCTACTGAAAAATGGCCAGTGGAATGACGTCCCCTGCTCCACCTCCCAT 785

Qy        721 CTGGCCGTCTGTGAGTTCCCTATCTGA 747
              ||||||||||||||||||||||||||
Db        786 CTGGCCGTCTGTGAGTTCCCTATCTGA 812
```

RESULT 13
ADR29057
ID ADR29057 standard; DNA; 1632 BP.
XX
AC ADR29057;
XX
DT 21-OCT-2004 (first entry)
XX
DE Human MBL gene with variant structural allele (in codon 57).
XX
KW Sepsis; septic shock; severe; MBL; mannose binding lectin; SIRS;
KW systemic inflammatory response syndrome; innate immune defence;
KW single nucleotide polymorphism; SNP; structural variant; regulatory;
KW prophylaxis; sepsis syndrome; infection susceptibility;
KW multiple organ failure; MOF; multiple organ dysfunction; acute; gene; ds;
KW human.
XX
OS Homo sapiens.
XX

FH	Key	Location/Qualifiers
FT	variation	1055
FT		/*tag= a
FT		/standard_name= "Single nucleotide polymorphism"
FT		/note= "Variant structural allele"

XX
PN WO2004065626-A2.
XX
PD 05-AUG-2004.
XX
PF 16-JAN-2004; 2004WO-DK000027.
XX
PR 17-JAN-2003; 2003DK-00000042.
PR 06-MAR-2003; 2003US-0453272P.
XX
PA (RIGS-) RIGSHOSPITALET.
PA (KOBE-) KOBENHAVNS AMT.
XX
PI Garred P, Madsen HO, Strom J;
XX
DR WPI; 2004-571694/55.
XX
PT Predicting whether an individual having Systemic Inflammatory Response
PT Syndrome (SIRS) will develop sepsis, useful for treating sepsis,
PT comprises determining the mannose-binding lectin (MBL) genotype or
PT concentration of MBL.
XX
PS Claim 3; SEQ ID NO 22; 65pp; English.
XX
CC The invention relates to a method to determine the risk factor of a
CC person for sepsis, severe sepsis or septic shock by correlating MBL
CC (mannose binding lectin) genotype with a predefined risk value. It
CC discloses the connection between the MBL genotype of an individual having
CC SIRS (Systemic Inflammatory Response Syndrome) and the risk of developing
CC sepsis, severe sepsis or septic shock. It shows how a decreased level of
CC MBL and lack of functional MBL are crucial to the development of sepsis
CC and septic shock in an individual having sepsis. A MBL is an important
CC factor in innate immune defence. MBL single nucleotide polymorphism in
CC the form of the structural variant (codon 54, codon 52 and codon 57) and
CC regulatory variant (low expression and high expression) were studied.
CC This invention discloses that the MBL gene polymorphism's causes a
CC reduction of the MBL level, which is associated with the development and
CC progression of sepsis in adult intensive care patients. The invention
CC offers a service to determine whether an individual belongs to a risk
CC group and it provides the treatment accordingly. There is an increased
CC risk of a fatal outcome of an individual carrying MBL variant alleles. A
CC rapid determination of MBL genotype of patients is important in
CC identifying individuals at risk of developing sepsis, severe sepsis or
CC septic shock. The MBL can be used for a medicament for the prevention and
CC treatment of specified diseases. The MBL variant allele is also
CC associated with an increased risk of death. It raises the prospective
CC that MBL (MBL substitution) can be used in prophylaxis and treatment of
CC sepsis syndrome. The frequency of MBL variant alleles is proportional to
CC the severity of sepsis which indicates lacking buffering capacity of MBL
CC towards initial microbial replication. It is not only associated with
CC susceptibility of infection but also allows activation of host mechanisms
CC central to the pathophysiology of the sepsis syndrome. The invention can
CC also predict the risk for developing multiple organ failure (MOF),
CC multiple organ dysfunction and acute organ dysfunction of an individual
CC having SIRS. The high risk is characterised by the presence of at least
CC one variant structural allele of the MBL gene and or having two low
CC expression regulatory alleles of the MBL gene in a sample. The presented
CC sequence is the variant structural allele (in codon 57) of MBL (mannose
CC binding lectin) gene from human.
XX
SQ Sequence 1632 BP; 448 A; 381 C; 429 G; 374 T; 0 U; 0 Other;

Query Match 99.8%; Score 745.4; DB 13; Length 1632;
Best Local Similarity 99.9%; Pred. No. 4.7e-207;
Matches 746; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
Qy          1 ATGTCCCTGTTTCCATCACTCCCTCTCCTTCTCCTGAGTATGGTGGCAGCGTCTTACTCA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        886 ATGTCCCTGTTTCCATCACTCCCTCTCCTTCTCCTGAGTATGGTGGCAGCGTCTTACTCA 945

Qy         61 GAAACTGTGACCTGTGAGGATGCCCAAAAGACCTGCCCTGCAGTGATTGCCTGTAGCTCT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        946 GAAACTGTGACCTGTGAGGATGCCCAAAAGACCTGCCCTGCAGTGATTGCCTGTAGCTCT 1005

Qy        121 CCAGGCATCAACGGCTTCCCAGGCAAAGATGGGCGTGATGGCACCAAGGGAGAAAAGGGG 180
              |||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||
Db       1006 CCAGGCATCAACGGCTTCCCAGGCAAAGATGGGCGTGATGGCACCAAGGAAGAAAAGGGG 1065

Qy        181 GAACCAGGCCAAGGGCTCAGAGGCTTACAGGGCCCCCCTGGAAAGTTGGGGCCTCCAGGA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1066 GAACCAGGCCAAGGGCTCAGAGGCTTACAGGGCCCCCCTGGAAAGTTGGGGCCTCCAGGA 1125

Qy        241 AATCCAGGGCCTTCTGGGTCACCAGGACCAAAGGGCCAAAAAGGAGACCCTGGAAAAAGT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1126 AATCCAGGGCCTTCTGGGTCACCAGGACCAAAGGGCCAAAAAGGAGACCCTGGAAAAAGT 1185

Qy        301 CCGGATGGTGATAGTAGCCTGGCTGCCTCAGAAAGAAAAGCTCTGCAAACAGAAATGGCA 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1186 CCGGATGGTGATAGTAGCCTGGCTGCCTCAGAAAGAAAAGCTCTGCAAACAGAAATGGCA 1245

Qy        361 CGTATCAAAAAGTGGCTGACCTTCTCTCTGGGCAAACAAGTTGGGAACAAGTTCTTCCTG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1246 CGTATCAAAAAGTGGCTGACCTTCTCTCTGGGCAAACAAGTTGGGAACAAGTTCTTCCTG 1305

Qy        421 ACCAATGGTGAAATAATGACCTTTGAAAAAGTGAAGGCCTTGTGTGTCAAGTTCCAGGCC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

```
Db       1306 ACCAATGGTGAAATAATGACCTTTGAAAAAGTGAAGGCCTTGTGTGTCAAGTTCCAGGCC 1365

Qy        481 TCTGTGGCCACCCCCAGGAATGCTGCAGAGAATGGAGCCATTCAGAATCTCATCAAGGAG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1366 TCTGTGGCCACCCCCAGGAATGCTGCAGAGAATGGAGCCATTCAGAATCTCATCAAGGAG 1425

Qy        541 GAAGCCTTCCTGGGCATCACTGATGAGAAGACAGAAGGGCAGTTTGTGGATCTGACAGGA 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1426 GAAGCCTTCCTGGGCATCACTGATGAGAAGACAGAAGGGCAGTTTGTGGATCTGACAGGA 1485

Qy        601 AATAGACTGACCTACACAAACTGGAACGAGGGTGAACCCAACAATGCTGGTTCTGATGAA 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1486 AATAGACTGACCTACACAAACTGGAACGAGGGTGAACCCAACAATGCTGGTTCTGATGAA 1545

Qy        661 GATTGTGTATTGCTACTGAAAAATGGCCAGTGGAATGACGTCCCCTGCTCCACCTCCCAT 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1546 GATTGTGTATTGCTACTGAAAAATGGCCAGTGGAATGACGTCCCCTGCTCCACCTCCCAT 1605

Qy        721 CTGGCCGTCTGTGAGTTCCCTATCTGA 747
              |||||||||||||||||||||||||||
Db       1606 CTGGCCGTCTGTGAGTTCCCTATCTGA 1632
```

RESULT 14
ADR29058
ID ADR29058 standard; DNA; 1638 BP.
XX
AC ADR29058;
XX
DT 21-OCT-2004 (first entry)
XX
DE Human MBL gene with variant structural allele (in codon 54).
XX
KW Sepsis; septic shock; severe; MBL; mannose binding lectin; SIRS;
KW systemic inflammatory response syndrome; innate immune defence;
KW single nucleotide polymorphism; SNP; structural variant; regulatory;
KW prophylaxis; sepsis syndrome; infection susceptibility;
KW multiple organ failure; MOF; multiple organ dysfunction; acute; gene; ds;
KW human.
XX
OS Homo sapiens.
XX
FH Key   Location/Qualifiers
FT variation   1052
FT   /*tag= a
FT   /standard_name= "Single nucleotide polymorphism"
FT   /note= "Variant structural allele"
XX
PN WO2004065626-A2.
XX
PD 05-AUG-2004.
XX
PF 16-JAN-2004; 2004WO-DK000027.
XX
PR 17-JAN-2003; 2003DK-00000042.
PR 06-MAR-2003; 2003US-0453272P.
XX
PA (RIGS-) RIGSHOSPITALET.
PA (KOBE-) KOBENHAVNS AMT.
XX
PI Garred P, Madsen HO, Strom J;
XX
DR WPI; 2004-571694/55.
XX
PT Predicting whether an individual having Systemic Inflammatory Response
PT Syndrome (SIRS) will develop sepsis, useful for treating sepsis,
PT comprises determining the mannose-binding lectin (MBL) genotype or
PT concentration of MBL.
XX
PS Claim 3; SEQ ID NO 23; 65pp; English.
XX
CC The invention relates to a method to determine the risk factor of a
CC person for sepsis, severe sepsis or septic shock by correlating MBL
CC (mannose binding lectin) genotype with a predefined risk value. It
CC discloses the connection between the MBL genotype of an individual having
CC SIRS (Systemic Inflammatory Response Syndrome) and the risk of developing
CC sepsis, severe sepsis or septic shock. It shows how a decreased level of
CC MBL and lack of functional MBL are crucial to the development of sepsis
CC and septic shock in an individual having sepsis. A MBL is an important
CC factor in innate immune defence. MBL single nucleotide polymorphism in
CC the form of the structural variant (codon 54, codon 52 and codon 57) and
CC regulatory variant (low expression and high expression) were studied.
CC This invention discloses that the MBL gene polymorphism's causes a
CC reduction of the MBL level, which is associated with the development and
CC progression of sepsis in adult intensive care patients. The invention
CC offers a service to determine whether an individual belongs to a risk
CC group and it provides the treatment accordingly. There is an increased
CC risk of a fatal outcome of an individual carrying MBL variant alleles. A
CC rapid determination of MBL genotype of patients is important in
CC identifying individuals at risk of developing sepsis, severe sepsis or
CC septic shock. The MBL can be used for a medicament for the prevention and
CC treatment of specified diseases. The MBL variant allele is also
CC associated with an increased risk of death. It raises the prospective
CC that MBL (MBL substitution) can be used in prophylaxis and treatment of
CC sepsis syndrome. The frequency of MBL variant alleles is proportional to
CC the severity of sepsis which indicates lacking buffering capacity of MBL
CC towards initial microbial replication. It is not only associated with
CC susceptibility of infection but also allows activation of host mechanisms
CC central to the pathophysiology of the sepsis syndrome. The invention can
CC also predict the risk for developing multiple organ failure (MOF),
CC multiple organ dysfunction and acute organ dysfunction of an individual
CC having SIRS. The high risk is characterised by the presence of at least
CC one variant structural allele of the MBL gene and or having two low
CC expression regulatory alleles of the MBL gene in a sample. The presented
CC sequence is human MBL gene with variant structural allele (in codon 54).
XX
SQ Sequence 1638 BP; 455 A; 382 C; 429 G; 372 T; 0 U; 0 Other;

  Query Match   99.8%; Score 745.4; DB 13; Length 1638;
  Best Local Similarity 99.9%; Pred. No. 4.7e-207;
  Matches 746; Conservative   0; Mismatches   1; Indels   0; Gaps   0;

```
Qy          1 ATGTCCCTGTTTCCATCACTCCCTCTCCTTCTCCTGAGTATGGTGGCAGCGTCTTACTCA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        892 ATGTCCCTGTTTCCATCACTCCCTCTCCTTCTCCTGAGTATGGTGGCAGCGTCTTACTCA 951

Qy         61 GAAACTGTGACCTGTGAGGATGCCCAAAAGACCTGCCCTGCAGTGATTGCCTGTAGCTCT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        952 GAAACTGTGACCTGTGAGGATGCCCAAAAGACCTGCCCTGCAGTGATTGCCTGTAGCTCT 1011

Qy        121 CCAGGCATCAACGGCTTCCCAGGCAAAGATGGGCGTGATGGCACCAAGGGAGAAAAGGGG 180
              |||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||
Db       1012 CCAGGCATCAACGGCTTCCCAGGCAAAGATGGGCGTGATGACACCAAGGGAGAAAAGGGG 1071

Qy        181 GAACCAGGCCAAGGGCTCAGAGGCTTACAGGGCCCCCCTGGAAAGTTGGGGCCTCCAGGA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1072 GAACCAGGCCAAGGGCTCAGAGGCTTACAGGGCCCCCCTGGAAAGTTGGGGCCTCCAGGA 1131

Qy        241 AATCCAGGGCCTTCTGGGTCACCAGGACCAAAGGGCCAAAAAGGAGACCCTGGAAAAAGT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1132 AATCCAGGGCCTTCTGGGTCACCAGGACCAAAGGGCCAAAAAGGAGACCCTGGAAAAAGT 1191

Qy        301 CCGGATGGTGATAGTAGCCTGGCTGCCTCAGAAAGAAAAGCTCTGCAAACAGAAATGGCA 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1192 CCGGATGGTGATAGTAGCCTGGCTGCCTCAGAAAGAAAAGCTCTGCAAACAGAAATGGCA 1251

Qy        361 CGTATCAAAAAGTGGCTGACCTTCTCTCTGGGCAAACAAGTTGGGAACAAGTTCTTCCTG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1252 CGTATCAAAAAGTGGCTGACCTTCTCTCTGGGCAAACAAGTTGGGAACAAGTTCTTCCTG 1311

Qy        421 ACCAATGGTGAAATAATGACCTTTGAAAAAGTGAAGGCCTTGTGTGTCAAGTTCCAGGCC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1312 ACCAATGGTGAAATAATGACCTTTGAAAAAGTGAAGGCCTTGTGTGTCAAGTTCCAGGCC 1371

Qy        481 TCTGTGGCCACCCCCAGGAATGCTGCAGAGAATGGAGCCATTCAGAATCTCATCAAGGAG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

```
Db       1372 TCTGTGGCCACCCCCAGGAATGCTGCAGAGAATGGAGCCATTCAGAATCTCATCAAGGAG 1431

Qy        541 GAAGCCTTCCTGGGCATCACTGATGAGAAGACAGAAGGGCAGTTTGTGGATCTGACAGGA 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1432 GAAGCCTTCCTGGGCATCACTGATGAGAAGACAGAAGGGCAGTTTGTGGATCTGACAGGA 1491

Qy        601 AATAGACTGACCTACACAAACTGGAACGAGGGTGAACCCAACAATGCTGGTTCTGATGAA 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1492 AATAGACTGACCTACACAAACTGGAACGAGGGTGAACCCAACAATGCTGGTTCTGATGAA 1551

Qy        661 GATTGTGTATTGCTACTGAAAAATGGCCAGTGGAATGACGTCCCCTGCTCCACCTCCCAT 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1552 GATTGTGTATTGCTACTGAAAAATGGCCAGTGGAATGACGTCCCCTGCTCCACCTCCCAT 1611

Qy        721 CTGGCCGTCTGTGAGTTCCCTATCTGA 747
              |||||||||||||||||||||||||||
Db       1612 CTGGCCGTCTGTGAGTTCCCTATCTGA 1638
```

RESULT 15
ADR29060
ID ADR29060 standard; DNA; 1638 BP.
XX
AC ADR29060;
XX
DT 21-OCT-2004 (first entry)
XX
DE Human MBL gene with non-structural/variant structural allele (codon 52).
XX
KW Sepsis; septic shock; severe; MBL; mannose binding lectin; SIRS;
KW systemic inflammatory response syndrome; innate immune defence;
KW single nucleotide polymorphism; SNP; structural variant; regulatory;
KW prophylaxis; sepsis syndrome; infection susceptibility;
KW multiple organ failure; MOF; multiple organ dysfunction; acute; gene; ds;
KW human.
XX
OS Homo sapiens.
XX
FH Key   Location/Qualifiers
FT variation   273
FT   /*tag= a
FT   /standard_name= "Single nucleotide polymorphism"
FT   /note= "Non-structural allele"
FT variation   1045
FT   /*tag= b
FT   /standard_name= "Single nucleotide polymorphism"
FT   /note= "Variant structural allele"
XX
PN WO2004065626-A2.
XX
PD 05-AUG-2004.
XX
PF 16-JAN-2004; 2004WO-DK000027.
XX
PR 17-JAN-2003; 2003DK-00000042.
PR 06-MAR-2003; 2003US-0453272P.
XX
PA (RIGS-) RIGSHOSPITALET.
PA (KOBE-) KOBENHAVNS AMT.
XX
PI Garred P, Madsen HO, Strom J;
XX
DR WPI; 2004-571694/55.
XX
PT Predicting whether an individual having Systemic Inflammatory Response
PT Syndrome (SIRS) will develop sepsis, useful for treating sepsis,
PT comprises determining the mannose-binding lectin (MBL) genotype or
PT concentration of MBL.
XX
PS Claim 3; SEQ ID NO 25; 65pp; English.
XX
CC The invention relates to a method to determine the risk factor of a
CC person for sepsis, severe sepsis or septic shock by correlating MBL
CC (mannose binding lectin) genotype with a predefined risk value. It
CC discloses the connection between the MBL genotype of an individual having
CC SIRS (Systemic Inflammatory Response Syndrome) and the risk of developing
CC sepsis, severe sepsis or septic shock. It shows how a decreased level of
CC MBL and lack of functional MBL are crucial to the development of sepsis
CC and septic shock in an individual having sepsis. A MBL is an important
CC factor in innate immune defence. MBL single nucleotide polymorphism in
CC the form of the structural variant (codon 54, codon 52 and codon 57) and
CC regulatory variant (low expression and high expression) were studied.
CC This invention discloses that the MBL gene polymorphism's causes a
CC reduction of the MBL level, which is associated with the development and
CC progression of sepsis in adult intensive care patients. The invention
CC offers a service to determine whether an individual belongs to a risk
CC group and it provides the treatment accordingly. There is an increased
CC risk of a fatal outcome of an individual carrying MBL variant alleles. A
CC rapid determination of MBL genotype of patients is important in
CC identifying individuals at risk of developing sepsis, severe sepsis or
CC septic shock. The MBL can be used for a medicament for the prevention and
CC treatment of specified diseases. The MBL variant allele is also
CC associated with an increased risk of death. It raises the prospective
CC that MBL (MBL substitution) can be used in prophylaxis and treatment of
CC sepsis syndrome. The frequency of MBL variant alleles is proportional to
CC the severity of sepsis which indicates lacking buffering capacity of MBL
CC towards initial microbial replication. It is not only associated with
CC susceptibility of infection but also allows activation of host mechanisms
CC central to the pathophysiology of the sepsis syndrome. The invention can
CC also predict the risk for developing multiple organ failure (MOF),
CC multiple organ dysfunction and acute organ dysfunction of an individual
CC having SIRS. The high risk is characterised by the presence of at least
CC one variant structural allele of the MBL gene and or having two low
CC expression regulatory alleles of the MBL gene in a sample. The presented
CC sequence is the human MBL gene with non-structural/variant structural
CC allele (in codon 52).
XX
SQ Sequence 1638 BP; 454 A; 380 C; 431 G; 373 T; 0 U; 0 Other;

```
  Query Match             99.8%;  Score 745.4;  DB 13;  Length 1638;
  Best Local Similarity   99.9%;  Pred. No. 4.7e-207;
  Matches  746;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 ATGTCCCTGTTTCCATCACTCCCTCTCCTTCTCCTGAGTATGGTGGCAGCGTCTTACTCA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        892 ATGTCCCTGTTTCCATCACTCCCTCTCCTTCTCCTGAGTATGGTGGCAGCGTCTTACTCA 951

Qy         61 GAAACTGTGACCTGTGAGGATGCCCAAAAGACCTGCCCTGCAGTGATTGCCTGTAGCTCT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        952 GAAACTGTGACCTGTGAGGATGCCCAAAAGACCTGCCCTGCAGTGATTGCCTGTAGCTCT 1011

Qy        121 CCAGGCATCAACGGCTTCCCAGGCAAAGATGGGCGTGATGGCACCAAGGGAGAAAAGGGG 180
              |||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||
Db       1012 CCAGGCATCAACGGCTTCCCAGGCAAAGATGGGTGTGATGGCACCAAGGGAGAAAAGGGG 1071

Qy        181 GAACCAGGCCAAGGGCTCAGAGGCTTACAGGGCCCCCCTGGAAAGTTGGGGCCTCCAGGA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1072 GAACCAGGCCAAGGGCTCAGAGGCTTACAGGGCCCCCCTGGAAAGTTGGGGCCTCCAGGA 1131

Qy        241 AATCCAGGGCCTTCTGGGTCACCAGGACCAAAGGGCCAAAAAGGAGACCCTGGAAAAAGT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1132 AATCCAGGGCCTTCTGGGTCACCAGGACCAAAGGGCCAAAAAGGAGACCCTGGAAAAAGT 1191

Qy        301 CCGGATGGTGATAGTAGCCTGGCTGCCTCAGAAAGAAAAGCTCTGCAAACAGAAATGGCA 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1192 CCGGATGGTGATAGTAGCCTGGCTGCCTCAGAAAGAAAAGCTCTGCAAACAGAAATGGCA 1251

Qy        361 CGTATCAAAAAGTGGCTGACCTTCTCTCTGGGCAAACAAGTTGGGAACAAGTTCTTCCTG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1252 CGTATCAAAAAGTGGCTGACCTTCTCTCTGGGCAAACAAGTTGGGAACAAGTTCTTCCTG 1311

Qy        421 ACCAATGGTGAAATAATGACCTTTGAAAAAGTGAAGGCCTTGTGTGTCAAGTTCCAGGCC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1312 ACCAATGGTGAAATAATGACCTTTGAAAAAGTGAAGGCCTTGTGTGTCAAGTTCCAGGCC 1371

Qy        481 TCTGTGGCCACCCCCAGGAATGCTGCAGAGAATGGAGCCATTCAGAATCTCATCAAGGAG 540
```

```
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1372 TCTGTGGCCACCCCCAGGAATGCTGCAGAGAATGGAGCCATTCAGAATCTCATCAAGGAG 1431

Qy        541 GAAGCCTTCCTGGGCATCACTGATGAGAAGACAGAAGGGCAGTTTGTGGATCTGACAGGA 600
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1432 GAAGCCTTCCTGGGCATCACTGATGAGAAGACAGAAGGGCAGTTTGTGGATCTGACAGGA 1491

Qy        601 AATAGACTGACCTACACAAACTGGAACGAGGGTGAACCCAACAATGCTGGTTCTGATGAA 660
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1492 AATAGACTGACCTACACAAACTGGAACGAGGGTGAACCCAACAATGCTGGTTCTGATGAA 1551

Qy        661 GATTGTGTATTGCTACTGAAAAATGGCCAGTGGAATGACGTCCCCTGCTCCACCTCCCAT 720
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1552 GATTGTGTATTGCTACTGAAAAATGGCCAGTGGAATGACGTCCCCTGCTCCACCTCCCAT 1611

Qy        721 CTGGCCGTCTGTGAGTTCCCTATCTGA 747
                ||||||||||||||||||||||||||
Db       1612 CTGGCCGTCTGTGAGTTCCCTATCTGA 1638
```

Search completed: June 20, 2005, 16:01:54
Job time : 545 secs

THIS PAGE BLANK (USPTO)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 19, 2005, 17:17:35 ; Search time 184 Seconds
(without alignments)
6642.928 Million cell updates/sec

Title: US-10-054-536-2
Perfect score: 747
Sequence: 1 atgtccctgtttccatcact.....tctgtgagttccctatctga 747

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_NA:*
1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	747	100.0	900	3	US-09-198-603C-1	Sequence 1, Appli
	2	747	100.0	1340	4	US-09-949-016-3499	Sequence 3499, Ap
	3	747	100.0	3605	4	US-09-949-016-36	Sequence 36, Appl
	4	374	50.1	8093	4	US-09-949-016-15241	Sequence 15241, A
	5	374	50.1	10320	4	US-09-949-016-11778	Sequence 11778, A
	6	204.4	27.4	1211	3	US-09-198-603C-25	Sequence 25, Appl
c	7	188	25.2	601	4	US-09-949-016-18336	Sequence 18336, A
c	8	188	25.2	601	4	US-09-949-016-124315	Sequence 124315,
	9	126	16.9	714	3	US-09-198-603C-26	Sequence 26, Appl
c	10	74	9.9	601	4	US-09-949-016-18337	Sequence 18337, A
c	11	74	9.9	601	4	US-09-949-016-124316	Sequence 124316,
	12	73.4	9.8	1558	3	US-09-198-603C-24	Sequence 24, Appl
c	13	72	9.6	601	4	US-09-949-016-18342	Sequence 18342, A
c	14	72	9.6	601	4	US-09-949-016-124321	Sequence 124321,
	15	67.6	9.0	885	1	US-08-365-103B-3	Sequence 3, Appli
	16	67.6	9.0	924	1	US-08-365-103B-5	Sequence 5, Appli
	17	67.6	9.0	1005	1	US-08-365-103B-1	Sequence 1, Appli
	18	63.4	8.5	747	4	US-09-949-016-741	Sequence 741, App
	19	62.8	8.4	369	3	US-09-535-521-24	Sequence 24, Appl
c	20	62.8	8.4	369	3	US-09-535-521-26	Sequence 26, Appl
	21	62.8	8.4	384	3	US-09-535-521-7	Sequence 7, Appli
c	22	62.8	8.4	384	3	US-09-535-521-9	Sequence 9, Appli
	23	62.8	8.4	417	3	US-09-535-521-10	Sequence 10, Appl
c	24	62.8	8.4	417	3	US-09-535-521-12	Sequence 12, Appl
	25	62.8	8.4	423	3	US-09-535-521-13	Sequence 13, Appl
c	26	62.8	8.4	423	3	US-09-535-521-15	Sequence 15, Appl
	27	62.8	8.4	561	3	US-09-535-521-16	Sequence 16, Appl
c	28	62.8	8.4	561	3	US-09-535-521-18	Sequence 18, Appl
	29	62.8	8.4	624	3	US-09-535-521-19	Sequence 19, Appl
c	30	62.8	8.4	624	3	US-09-535-521-21	Sequence 21, Appl
	31	62.8	8.4	876	3	US-09-535-521-4	Sequence 4, Appli
c	32	62.8	8.4	876	3	US-09-535-521-6	Sequence 6, Appli
	33	62.8	8.4	2851	3	US-09-535-521-1	Sequence 1, Appli
c	34	62.8	8.4	2851	3	US-09-535-521-3	Sequence 3, Appli
	35	61.8	8.3	1412	4	US-09-949-016-2610	Sequence 2610, Ap
	36	61.8	8.3	1412	4	US-09-949-016-3187	Sequence 3187, Ap
	37	60.2	8.1	1413	4	US-09-949-016-3188	Sequence 3188, Ap
	38	60.2	8.1	6288	4	US-09-949-016-12483	Sequence 12483, A
	39	60.2	8.1	7948	4	US-09-949-016-14929	Sequence 14929, A
	40	60.2	8.1	7950	4	US-09-949-016-14352	Sequence 14352, A
c	41	58.6	7.8	601	4	US-09-949-016-32278	Sequence 32278, A
c	42	58.6	7.8	601	4	US-09-949-016-116481	Sequence 116481,
	43	58.6	7.8	7960	4	US-09-949-016-14930	Sequence 14930, A
	44	55.4	7.4	2891	4	US-09-949-016-3019	Sequence 3019, Ap
	45	55.4	7.4	8050	4	US-09-949-016-12	Sequence 12, Appl

ALIGNMENTS

RESULT 1
US-09-198-603C-1
; Sequence 1, Application US/09198603C
; Patent No. 6337193
; GENERAL INFORMATION:
; APPLICANT: TULLY, Raymond E.
; APPLICANT: CALTAGIRONE, G. Thomas
; APPLICANT: MOYER, Shawn S.
; APPLICANT: RONNING, Michael T.
; TITLE OF INVENTION: EXPRESSION OF MANNOSE-BINDING PROTEIN IN METHYLOTROPHIC
; TITLE OF INVENTION: YEAST
; FILE REFERENCE: A7290
; CURRENT APPLICATION NUMBER: US/09/198,603C
; CURRENT FILING DATE: 1998-11-24
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 900
; TYPE: DNA
; ORGANISM: Human
US-09-198-603C-1

Query Match 100.0%; Score 747; DB 3; Length 900;
Best Local Similarity 100.0%; Pred. No. 2.1e-227;
Matches 747; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 ATGTCCCTGTTTCCATCACTCCCTCTCCTTCTCCTGAGTATGGTGGCAGCGTCTTACTCA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         66 ATGTCCCTGTTTCCATCACTCCCTCTCCTTCTCCTGAGTATGGTGGCAGCGTCTTACTCA 125

Qy         61 GAAACTGTGACCTGTGAGGATGCCCAAAAGACCTGCCCTGCAGTGATTGCCTGTAGCTCT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        126 GAAACTGTGACCTGTGAGGATGCCCAAAAGACCTGCCCTGCAGTGATTGCCTGTAGCTCT 185

Qy        121 CCAGGCATCAACGGCTTCCCAGGCAAAGATGGGCGTGATGGCACCAAGGGAGAAAAGGGG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        186 CCAGGCATCAACGGCTTCCCAGGCAAAGATGGGCGTGATGGCACCAAGGGAGAAAAGGGG 245

Qy        181 GAACCAGGCCAAGGGCTCAGAGGCTTACAGGGCCCCCCTGGAAAGTTGGGGCCTCCAGGA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        246 GAACCAGGCCAAGGGCTCAGAGGCTTACAGGGCCCCCCTGGAAAGTTGGGGCCTCCAGGA 305

Qy        241 AATCCAGGGCCTTCTGGGTCACCAGGACCAAAGGGCCAAAAAGGAGACCCTGGAAAAAGT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        306 AATCCAGGGCCTTCTGGGTCACCAGGACCAAAGGGCCAAAAAGGAGACCCTGGAAAAAGT 365

Qy        301 CCGGATGGTGATAGTAGCCTGGCTGCCTCAGAAAGAAAAGCTCTGCAAACAGAAATGGCA 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        366 CCGGATGGTGATAGTAGCCTGGCTGCCTCAGAAAGAAAAGCTCTGCAAACAGAAATGGCA 425
```

```
Qy        361 CGTATCAAAAAGTGGCTGACCTTCTCTCTGGGCAAACAAGTTGGGAACAAGTTCTTCCTG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        426 CGTATCAAAAAGTGGCTGACCTTCTCTCTGGGCAAACAAGTTGGGAACAAGTTCTTCCTG 485

Qy        421 ACCAATGGTGAAATAATGACCTTTGAAAAAGTGAAGGCCTTGTGTGTCAAGTTCCAGGCC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        486 ACCAATGGTGAAATAATGACCTTTGAAAAAGTGAAGGCCTTGTGTGTCAAGTTCCAGGCC 545

Qy        481 TCTGTGGCCACCCCCAGGAATGCTGCAGAGAATGGAGCCATTCAGAATCTCATCAAGGAG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        546 TCTGTGGCCACCCCCAGGAATGCTGCAGAGAATGGAGCCATTCAGAATCTCATCAAGGAG 605

Qy        541 GAAGCCTTCCTGGGCATCACTGATGAGAAGACAGAAGGGCAGTTTGTGGATCTGACAGGA 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        606 GAAGCCTTCCTGGGCATCACTGATGAGAAGACAGAAGGGCAGTTTGTGGATCTGACAGGA 665

Qy        601 AATAGACTGACCTACACAAACTGGAACGAGGGTGAACCCAACAATGCTGGTTCTGATGAA 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        666 AATAGACTGACCTACACAAACTGGAACGAGGGTGAACCCAACAATGCTGGTTCTGATGAA 725

Qy        661 GATTGTGTATTGCTACTGAAAAATGGCCAGTGGAATGACGTCCCCTGCTCCACCTCCCAT 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        726 GATTGTGTATTGCTACTGAAAAATGGCCAGTGGAATGACGTCCCCTGCTCCACCTCCCAT 785

Qy        721 CTGGCCGTCTGTGAGTTCCCTATCTGA 747
              |||||||||||||||||||||||||||
Db        786 CTGGCCGTCTGTGAGTTCCCTATCTGA 812
```

RESULT 2
US-09-949-016-3499
; Sequence 3499, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3499
; LENGTH: 1340
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-3499

Query Match 100.0%; Score 747; DB 4; Length 1340;
Best Local Similarity 100.0%; Pred. No. 2.6e-227;
Matches 747; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 ATGTCCCTGTTTCCATCACTCCCTCTCCTTCTCCTGAGTATGGTGGCAGCGTCTTACTCA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         66 ATGTCCCTGTTTCCATCACTCCCTCTCCTTCTCCTGAGTATGGTGGCAGCGTCTTACTCA 125

Qy         61 GAAACTGTGACCTGTGAGGATGCCCAAAAGACCTGCCCTGCAGTGATTGCCTGTAGCTCT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        126 GAAACTGTGACCTGTGAGGATGCCCAAAAGACCTGCCCTGCAGTGATTGCCTGTAGCTCT 185

Qy        121 CCAGGCATCAACGGCTTCCCAGGCAAAGATGGGCGTGATGGCACCAAGGGAGAAAAGGGG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        186 CCAGGCATCAACGGCTTCCCAGGCAAAGATGGGCGTGATGGCACCAAGGGAGAAAAGGGG 245

Qy        181 GAACCAGGCCAAGGGCTCAGAGGCTTACAGGGCCCCCCTGGAAAGTTGGGGCCTCCAGGA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        246 GAACCAGGCCAAGGGCTCAGAGGCTTACAGGGCCCCCCTGGAAAGTTGGGGCCTCCAGGA 305

Qy        241 AATCCAGGGCCTTCTGGGTCACCAGGACCAAAGGGCCAAAAAGGAGACCCTGGAAAAAGT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        306 AATCCAGGGCCTTCTGGGTCACCAGGACCAAAGGGCCAAAAAGGAGACCCTGGAAAAAGT 365

Qy        301 CCGGATGGTGATAGTAGCCTGGCTGCCTCAGAAAGAAAAGCTCTGCAAACAGAAATGGCA 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        366 CCGGATGGTGATAGTAGCCTGGCTGCCTCAGAAAGAAAAGCTCTGCAAACAGAAATGGCA 425

Qy        361 CGTATCAAAAAGTGGCTGACCTTCTCTCTGGGCAAACAAGTTGGGAACAAGTTCTTCCTG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        426 CGTATCAAAAAGTGGCTGACCTTCTCTCTGGGCAAACAAGTTGGGAACAAGTTCTTCCTG 485

Qy        421 ACCAATGGTGAAATAATGACCTTTGAAAAAGTGAAGGCCTTGTGTGTCAAGTTCCAGGCC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        486 ACCAATGGTGAAATAATGACCTTTGAAAAAGTGAAGGCCTTGTGTGTCAAGTTCCAGGCC 545

Qy        481 TCTGTGGCCACCCCCAGGAATGCTGCAGAGAATGGAGCCATTCAGAATCTCATCAAGGAG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        546 TCTGTGGCCACCCCCAGGAATGCTGCAGAGAATGGAGCCATTCAGAATCTCATCAAGGAG 605

Qy        541 GAAGCCTTCCTGGGCATCACTGATGAGAAGACAGAAGGGCAGTTTGTGGATCTGACAGGA 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        606 GAAGCCTTCCTGGGCATCACTGATGAGAAGACAGAAGGGCAGTTTGTGGATCTGACAGGA 665

Qy        601 AATAGACTGACCTACACAAACTGGAACGAGGGTGAACCCAACAATGCTGGTTCTGATGAA 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        666 AATAGACTGACCTACACAAACTGGAACGAGGGTGAACCCAACAATGCTGGTTCTGATGAA 725

Qy        661 GATTGTGTATTGCTACTGAAAAATGGCCAGTGGAATGACGTCCCCTGCTCCACCTCCCAT 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        726 GATTGTGTATTGCTACTGAAAAATGGCCAGTGGAATGACGTCCCCTGCTCCACCTCCCAT 785

Qy        721 CTGGCCGTCTGTGAGTTCCCTATCTGA 747
              |||||||||||||||||||||||||||
Db        786 CTGGCCGTCTGTGAGTTCCCTATCTGA 812
```

RESULT 3
US-09-949-016-36
; Sequence 36, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 36
; LENGTH: 3605
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-36

Query Match 100.0%; Score 747; DB 4; Length 3605;
Best Local Similarity 100.0%; Pred. No. 4.6e-227;
Matches 747; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 ATGTCCCTGTTTCCATCACTCCCTCTCCTTCTCCTGAGTATGGTGGCAGCGTCTTACTCA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         66 ATGTCCCTGTTTCCATCACTCCCTCTCCTTCTCCTGAGTATGGTGGCAGCGTCTTACTCA 125

Qy         61 GAAACTGTGACCTGTGAGGATGCCCAAAAGACCTGCCCTGCAGTGATTGCCTGTAGCTCT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

```
Db        126 GAAACTGTGACCTGTGAGGATGCCCAAAAGACCTGCCCTGCAGTGATTGCCTGTAGCTCT 185

Qy        121 CCAGGCATCAACGGCTTCCCAGGCAAAGATGGGCGTGATGGCACCAAGGGAGAAAAGGGG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        186 CCAGGCATCAACGGCTTCCCAGGCAAAGATGGGCGTGATGGCACCAAGGGAGAAAAGGGG 245

Qy        181 GAACCAGGCCAAGGGCTCAGAGGCTTACAGGGCCCCCCTGGAAAGTTGGGGCCTCCAGGA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        246 GAACCAGGCCAAGGGCTCAGAGGCTTACAGGGCCCCCCTGGAAAGTTGGGGCCTCCAGGA 305

Qy        241 AATCCAGGGCCTTCTGGGTCACCAGGACCAAAGGGCCAAAAAGGAGACCCTGGAAAAAGT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        306 AATCCAGGGCCTTCTGGGTCACCAGGACCAAAGGGCCAAAAAGGAGACCCTGGAAAAAGT 365

Qy        301 CCGGATGGTGATAGTAGCCTGGCTGCCTCAGAAAGAAAAGCTCTGCAAACAGAAATGGCA 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        366 CCGGATGGTGATAGTAGCCTGGCTGCCTCAGAAAGAAAAGCTCTGCAAACAGAAATGGCA 425

Qy        361 CGTATCAAAAAGTGGCTGACCTTCTCTCTGGGCAAACAAGTTGGGAACAAGTTCTTCCTG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        426 CGTATCAAAAAGTGGCTGACCTTCTCTCTGGGCAAACAAGTTGGGAACAAGTTCTTCCTG 485

Qy        421 ACCAATGGTGAAATAATGACCTTTGAAAAAGTGAAGGCCTTGTGTGTCAAGTTCCAGGCC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        486 ACCAATGGTGAAATAATGACCTTTGAAAAAGTGAAGGCCTTGTGTGTCAAGTTCCAGGCC 545

Qy        481 TCTGTGGCCACCCCCAGGAATGCTGCAGAGAATGGAGCCATTCAGAATCTCATCAAGGAG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        546 TCTGTGGCCACCCCCAGGAATGCTGCAGAGAATGGAGCCATTCAGAATCTCATCAAGGAG 605

Qy        541 GAAGCCTTCCTGGGCATCACTGATGAGAAGACAGAAGGGCAGTTTGTGGATCTGACAGGA 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        606 GAAGCCTTCCTGGGCATCACTGATGAGAAGACAGAAGGGCAGTTTGTGGATCTGACAGGA 665

Qy        601 AATAGACTGACCTACACAAACTGGAACGAGGGTGAACCCAACAATGCTGGTTCTGATGAA 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        666 AATAGACTGACCTACACAAACTGGAACGAGGGTGAACCCAACAATGCTGGTTCTGATGAA 725

Qy        661 GATTGTGTATTGCTACTGAAAAATGGCCAGTGGAATGACGTCCCCTGCTCCACCTCCCAT 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        726 GATTGTGTATTGCTACTGAAAAATGGCCAGTGGAATGACGTCCCCTGCTCCACCTCCCAT 785

Qy        721 CTGGCCGTCTGTGAGTTCCCTATCTGA 747
              |||||||||||||||||||||||||||
Db        786 CTGGCCGTCTGTGAGTTCCCTATCTGA 812


RESULT 4
US-09-949-016-15241
; Sequence 15241, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 15241
;   LENGTH: 8093
;   TYPE: DNA
;   ORGANISM: Human
US-09-949-016-15241

  Query Match             50.1%;  Score 374;  DB 4;  Length 8093;
  Best Local Similarity   100.0%;  Pred. No. 4.8e-108;
  Matches  374;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         374 GGCTGACCTTCTCTCTGGGCAAACAAGTTGGGAACAAGTTCTTCCTGACCAATGGTGAAA 433
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        5191 GGCTGACCTTCTCTCTGGGCAAACAAGTTGGGAACAAGTTCTTCCTGACCAATGGTGAAA 5250

Qy         434 TAATGACCTTTGAAAAAGTGAAGGCCTTGTGTGTCAAGTTCCAGGCCTCTGTGGCCACCC 493
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        5251 TAATGACCTTTGAAAAAGTGAAGGCCTTGTGTGTCAAGTTCCAGGCCTCTGTGGCCACCC 5310

Qy         494 CCAGGAATGCTGCAGAGAATGGAGCCATTCAGAATCTCATCAAGGAGGAAGCCTTCCTGG 553
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        5311 CCAGGAATGCTGCAGAGAATGGAGCCATTCAGAATCTCATCAAGGAGGAAGCCTTCCTGG 5370

Qy         554 GCATCACTGATGAGAAGACAGAAGGGCAGTTTGTGGATCTGACAGGAAATAGACTGACCT 613
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        5371 GCATCACTGATGAGAAGACAGAAGGGCAGTTTGTGGATCTGACAGGAAATAGACTGACCT 5430

Qy         614 ACACAAACTGGAACGAGGGTGAACCCAACAATGCTGGTTCTGATGAAGATTGTGTATTGC 673
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        5431 ACACAAACTGGAACGAGGGTGAACCCAACAATGCTGGTTCTGATGAAGATTGTGTATTGC 5490

Qy         674 TACTGAAAAATGGCCAGTGGAATGACGTCCCCTGCTCCACCTCCCATCTGGCCGTCTGTG 733
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        5491 TACTGAAAAATGGCCAGTGGAATGACGTCCCCTGCTCCACCTCCCATCTGGCCGTCTGTG 5550

Qy         734 AGTTCCCTATCTGA 747
               ||||||||||||||
Db        5551 AGTTCCCTATCTGA 5564


RESULT 5
US-09-949-016-11778
; Sequence 11778, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 11778
;   LENGTH: 10320
;   TYPE: DNA
;   ORGANISM: Human
US-09-949-016-11778

  Query Match             50.1%;  Score 374;  DB 4;  Length 10320;
  Best Local Similarity   100.0%;  Pred. No. 5.5e-108;
  Matches  374;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         374 GGCTGACCTTCTCTCTGGGCAAACAAGTTGGGAACAAGTTCTTCCTGACCAATGGTGAAA 433
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        5191 GGCTGACCTTCTCTCTGGGCAAACAAGTTGGGAACAAGTTCTTCCTGACCAATGGTGAAA 5250

Qy         434 TAATGACCTTTGAAAAAGTGAAGGCCTTGTGTGTCAAGTTCCAGGCCTCTGTGGCCACCC 493
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        5251 TAATGACCTTTGAAAAAGTGAAGGCCTTGTGTGTCAAGTTCCAGGCCTCTGTGGCCACCC 5310

Qy         494 CCAGGAATGCTGCAGAGAATGGAGCCATTCAGAATCTCATCAAGGAGGAAGCCTTCCTGG 553
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        5311 CCAGGAATGCTGCAGAGAATGGAGCCATTCAGAATCTCATCAAGGAGGAAGCCTTCCTGG 5370
```

```
Qy        554 GCATCACTGATGAGAAGACAGAAGGGCAGTTTGTGGATCTGACAGGAAATAGACTGACCT 613
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5371 GCATCACTGATGAGAAGACAGAAGGGCAGTTTGTGGATCTGACAGGAAATAGACTGACCT 5430

Qy        614 ACACAAACTGGAACGAGGGTGAACCCAACAATGCTGGTTCTGATGAAGATTGTGTATTGC 673
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5431 ACACAAACTGGAACGAGGGTGAACCCAACAATGCTGGTTCTGATGAAGATTGTGTATTGC 5490

Qy        674 TACTGAAAAATGGCCAGTGGAATGACGTCCCCTGCTCCACCTCCCATCTGGCCGTCTGTG 733
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5491 TACTGAAAAATGGCCAGTGGAATGACGTCCCCTGCTCCACCTCCCATCTGGCCGTCTGTG 5550

Qy        734 AGTTCCCTATCTGA 747
              ||||||||||||||
Db       5551 AGTTCCCTATCTGA 5564
```

RESULT 6
US-09-198-603C-25
; Sequence 25, Application US/09198603C
; Patent No. 6337193
; GENERAL INFORMATION:
; APPLICANT: TULLY, Raymond E.
; APPLICANT: CALTAGIRONE, G. Thomas
; APPLICANT: MOYER, Shawn S.
; APPLICANT: RONNING, Michael T.
; TITLE OF INVENTION: EXPRESSION OF MANNOSE-BINDING PROTEIN IN METHYLOTROPHIC
; TITLE OF INVENTION: YEAST
; FILE REFERENCE: A7290
; CURRENT APPLICATION NUMBER: US/09/198,603C
; CURRENT FILING DATE: 1998-11-24
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 25
; LENGTH: 1211
; TYPE: DNA
; ORGANISM: Mouse
US-09-198-603C-25

Query Match 27.4%; Score 204.4; DB 3; Length 1211;
Best Local Similarity 71.7%; Pred. No. 1.7e-54;
Matches 268; Conservative 0; Mismatches 106; Indels 0; Gaps 0;

```
Qy        374 GGCTGACCTTCTCTCTGGGCAAACAAGTTGGGAACAAGTTCTTCCTGACCAATGGTGAAA 433
              || ||  |||||||||| |  || |||||| || ||||  ||  ||| || || | |||
Db        576 GGGTGCTCTTCTCTCTGAGTGAAAAAGTTGGAAAGAAGTATTTTGTGAGCAGTGTTAAAA 635

Qy        434 TAATGACCTTTGAAAAAGTGAAGGCCTTGTGTGTCAAGTTCCAGGCCTCTGTGGCCACCC 493
              ||||  | ||||  | |||||||||| ||||    | | ||||||| ||||||||||| |
Db        636 AGATGAGCCTTGATAGAGTGAAGGCCCTGTGCTCCGAATTCCAGGGCTCTGTGGCCACTC 695

Qy        494 CCAGGAATGCTGCAGAGAATGGAGCCATTCAGAATCTCATCAAGGAGGAAGCCTTCCTGG 553
              ||||||||||||  || ||    ||||| |||||  |   ||| ||    |||| | |||
Db        696 CCAGGAATGCTGAGGAAAACTCGGCCATCCAGAAAGTGGCCAAAGATATTGCCTACTTGG 755

Qy        554 GCATCACTGATGAGAAGACAGAAGGGCAGTTTGTGGATCTGACAGGAAATAGACTGACCT 613
              ||||||| |||| || |   |||||     |||| |||||||||||||| ||| ||  ||
Db        756 GCATCACAGATGTGAGGGTTGAAGGCAGTTTTGAGGATCTGACAGGAAACAGAGTGCGCT 815

Qy        614 ACACAAACTGGAACGAGGGTGAACCCAACAATGCTGGTTCTGATGAAGATTGTGTATTGC 673
              | || || ||||| || || || ||||||||  | ||   ||  |||||  |||||  ||
Db        816 ATACTAATTGGAATGATGGGGAGCCCAACAACACGGGCGATGGGGAAGACTGTGTGGTGA 875

Qy        674 TACTGAAAAATGGCCAGTGGAATGACGTCCCCTGCTCCACCTCCCATCTGGCCGTCTGTG 733
              |  ||  ||||||| ||||||| || ||||||||||   |||   | ||||  | ||||
Db        876 TCTTGGGAAATGGCAAGTGGAACGATGTCCCCTGCTCTGACTCTTTTTTGGCAATATGTG 935

Qy        734 AGTTCCCTATCTGA 747
              | ||| ||  ||||
Db        936 AATTCTCTGACTGA 949
```

RESULT 7

US-09-949-016-18336/c
; Sequence 18336, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 18336
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-18336

Query Match 25.2%; Score 188; DB 4; Length 601;
Best Local Similarity 100.0%; Pred. No. 1.9e-49;
Matches 188; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 ATGTCCCTGTTTCCATCACTCCCTCTCCTTCTCCTGAGTATGGTGGCAGCGTCTTACTCA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        597 ATGTCCCTGTTTCCATCACTCCCTCTCCTTCTCCTGAGTATGGTGGCAGCGTCTTACTCA 538

Qy         61 GAAACTGTGACCTGTGAGGATGCCCAAAAGACCTGCCCTGCAGTGATTGCCTGTAGCTCT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        537 GAAACTGTGACCTGTGAGGATGCCCAAAAGACCTGCCCTGCAGTGATTGCCTGTAGCTCT 478

Qy        121 CCAGGCATCAACGGCTTCCCAGGCAAAGATGGGCGTGATGGCACCAAGGGAGAAAAGGGG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        477 CCAGGCATCAACGGCTTCCCAGGCAAAGATGGGCGTGATGGCACCAAGGGAGAAAAGGGG 418

Qy        181 GAACCAGG 188
              ||||||||
Db        417 GAACCAGG 410
```

RESULT 8
US-09-949-016-124315/c
; Sequence 124315, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 124315
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-124315

Query Match 25.2%; Score 188; DB 4; Length 601;
Best Local Similarity 100.0%; Pred. No. 1.9e-49;
Matches 188; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 ATGTCCCTGTTTCCATCACTCCCTCTCCTTCTCCTGAGTATGGTGGCAGCGTCTTACTCA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        597 ATGTCCCTGTTTCCATCACTCCCTCTCCTTCTCCTGAGTATGGTGGCAGCGTCTTACTCA 538

Qy         61 GAAACTGTGACCTGTGAGGATGCCCAAAAGACCTGCCCTGCAGTGATTGCCTGTAGCTCT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        537 GAAACTGTGACCTGTGAGGATGCCCAAAAGACCTGCCCTGCAGTGATTGCCTGTAGCTCT 478

Qy        121 CCAGGCATCAACGGCTTCCCAGGCAAAGATGGGCGTGATGGCACCAAGGGAGAAAAGGGG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        477 CCAGGCATCAACGGCTTCCCAGGCAAAGATGGGCGTGATGGCACCAAGGGAGAAAAGGGG 418

Qy        181 GAACCAGG 188
              ||||||||
Db        417 GAACCAGG 410
```

RESULT 9
US-09-198-603C-26
; Sequence 26, Application US/09198603C
; Patent No. 6337193
; GENERAL INFORMATION:
; APPLICANT: TULLY, Raymond E.
; APPLICANT: CALTAGIRONE, G. Thomas
; APPLICANT: MOYER, Shawn S.
; APPLICANT: RONNING, Michael T.
; TITLE OF INVENTION: EXPRESSION OF MANNOSE-BINDING PROTEIN IN METHYLOTROPHIC
; TITLE OF INVENTION: YEAST
; FILE REFERENCE: A7290.
; CURRENT APPLICATION NUMBER: US/09/198,603C
; CURRENT FILING DATE: 1998-11-24
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 26
; LENGTH: 714
; TYPE: DNA
; ORGANISM: CHICKEN
US-09-198-603C-26

Query Match 16.9%; Score 126; DB 3; Length 714;
Best Local Similarity 53.0%; Pred. No. 1.2e-29;
Matches 351; Conservative 0; Mismatches 290; Indels 21; Gaps 3;

```
Qy         79 GATGCCCAAAAGACCTGCCCTGCAGTGATTGCCTGTAGCTCTCCAGGCATCAACGGCTTC 138
              || |   ||| |   | |  | |  | |||   |||||  ||||  |   ||||  || ||
Db         37 GAAGAGAAAATGTATTCCTGTCCCATCATTCAGTGTAGTGCTCCTGCAGTCAATGGATTA 96

Qy        139 CCAGGCAAAGATGGGCGTGATGGCACCAAGGGAGAAAAGGGGGAACCAGGCCAAGGGCTC 198
              |||||||  ||||||  | |||||  ||||  ||  ||||||||  ||  |||||  ||||  ||
Db         97 CCAGGCAGAGATGGAAGAGATGGTCCCAAAGGGGAAAAGGGAGACCCAGGAGAAGGACTG 156

Qy        199 AGAGGCTTACAGGGCCCCCCTGGAAAGTTGGGGCCTCCAGGAAATCCAGGGCCTTCTGGG 258
              |||||  | |||||    |||||||||    ||  ||  | ||||     |||        ||
Db        157 AGAGGTCTGCAGGGTTTGCCTGGAAAAGCAGGACCCCAAGGATTAAAAGGAGAGGTGGGA 216

Qy        259 TCACCAGGACCAAAGGGCCAAAAAGGAGACCCTGGAA----------AAAGTCCGGAT 306
              |||  ||||   ||  ||  ||||||||||  | |||||          |   | | |
Db        217 CCACAAGGAGAGAAAGGTCAAAAAGGAGAACGTGGAATTGTTGTAACTGATGACCTGCAC 276

Qy        307 GGTGATAGTAGCCTGGCTGCCTCAGAAAGAAAAGCTCTGCAAACAGAAATGGCACGTATC 366
              |  | | |        |   || |||    |   || ||   ||  |    |   |
Db        277 CGACAAATAACTGATTTGGAAGCAAAAATCCGGGTATTGGAAGATGACTTAAGCAGATAC 336

Qy        367 AAAAAGTGGCTGACCTTCTCTCTGGGCAAACAAGTTGGGAACAAGTTCTTCCTGACCAAT 426
              |||||     |||  ||       | |  | |  |||| || ||  | ||  |  | | |
Db        337 AAAAAAGCCTTGAGTTTAAAGGACGTCGTAAACATTGGTAAAAAAATGTTTGTCTCAACT 396

Qy        427 GGTGAAATAATGACCTTTGAAAAAGTGAAGGCCTTGTGTGTCAAGTTCCAGGCCTCTGTG 486
              ||  | | |   | ||||||| |  ||  || | ||||  ||          |
Db        397 GGAAAGAAATATAATTTTGAAAAGGGAAAATCCCTTTGTGCAAAAGCTGGAAGTGTGCTT 456

Qy        487 GCCACCCCCAGGAATGCTGCAGAGAATGGAGCCATTCAGAATCTCATCAAG------GAG 540
              ||| | || ||||| |  || ||||||  |||  |  |  |  | ||  |
Db        457 GCCTCTCCTAGGAACGAGGCTGAGAATACAGCTTTAAAAGACTTAATTGACCCTTCAAGC 516

Qy        541 GAAGCCTTCCTGGGCATCACTGATGAGAAGACAGAAGGGCAGTTTGTGGATCTGACAGGA 600
              ||||  |   | ||  ||  ||||||   | ||  ||  ||    ||  ||  | ||||  ||
Db        517 CAAGCTTATATTGGGATATCTGATGCACAAACTGAGGGCAGATTCATGTACCTGAGTGGT 576

Qy        601 AATAGACTGACCTACACAAACTGGAACGAGGGTGAACCCAACAATGCTGGTTCTGATGAA 660
              | ||  |||| |||||||    ||  |||||  ||  |||          |||||
Db        577 GGGCCTTTAACTTACAGCAACTGGAAACCTGGAGAACCAAATAATCACAAAA---ATGAA 633

Qy        661 GATTGTGTATTGCTACTGAAAAATGGCCAGTGGAATGACGTCCCCTGCTCCACCTCCCAT 720
              ||  ||||   ||  ||    |   |||  | |||||||||  |   |||  ||  |  ||
Db        634 GACTGTGCGGTGATAGAAGACTCTGGAAAATGGAATGATTTAGACTGTTCAAATTCAAAT 693

Qy        721 CT 722
              |
Db        694 AT 695
```

RESULT 10
US-09-949-016-18337/c
; Sequence 18337, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 18337
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-18337

Query Match 9.9%; Score 74; DB 4; Length 601;
Best Local Similarity 100.0%; Pred. No. 4e-13;
Matches 74; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy        115 AGCTCTCCAGGCATCAACGGCTTCCCAGGCAAAGATGGGCGTGATGGCACCAAGGGAGAA 174
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 AGCTCTCCAGGCATCAACGGCTTCCCAGGCAAAGATGGGCGTGATGGCACCAAGGGAGAA 542

Qy        175 AAGGGGGAACCAGG 188
              ||||||||||||||
Db        541 AAGGGGGAACCAGG 528
```

RESULT 11
US-09-949-016-124316/c
; Sequence 124316, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03

```
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 124316
;    LENGTH: 601
;    TYPE: DNA
;    ORGANISM: Human
US-09-949-016-124316

  Query Match              9.9%;  Score 74;  DB 4;  Length 601;
  Best Local Similarity   100.0%;  Pred. No. 4e-13;
  Matches   74;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        115 AGCTCTCCAGGCATCAACGGCTTCCCAGGCAAAGATGGGCGTGATGGCACCAAGGGAGAA 174
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 AGCTCTCCAGGCATCAACGGCTTCCCAGGCAAAGATGGGCGTGATGGCACCAAGGGAGAA 542

Qy        175 AAGGGGGAACCAGG 188
              ||||||||||||||
Db        541 AAGGGGGAACCAGG 528


RESULT 12
US-09-198-603C-24
; Sequence 24, Application US/09198603C
; Patent No. 6337193
; GENERAL INFORMATION:
;  APPLICANT:  TULLY, Raymond E.
;  APPLICANT:  CALTAGIRONE, G. Thomas
;  APPLICANT:  MOYER, Shawn S.
;  APPLICANT:  RONNING, Michael T.
;  TITLE OF INVENTION:  EXPRESSION OF MANNOSE-BINDING PROTEIN IN METHYLOTROPHIC
;  TITLE OF INVENTION:  YEAST
;  FILE REFERENCE:  A7290
;  CURRENT APPLICATION NUMBER: US/09/198,603C
;  CURRENT FILING DATE:  1998-11-24
;  NUMBER OF SEQ ID NOS:  26
;  SOFTWARE:  PatentIn Ver. 2.1
; SEQ ID NO 24
;    LENGTH: 1558
;    TYPE: DNA
;    ORGANISM: RAT
US-09-198-603C-24

  Query Match              9.8%;  Score 73.4;  DB 3;  Length 1558;
  Best Local Similarity   77.4%;  Pred. No. 1.1e-12;
  Matches   89;  Conservative    0;  Mismatches   26;  Indels    0;  Gaps    0;

Qy        185 CAGGCCAAGGGCTCAGAGGCTTACAGGGCCCCCCTGGAAAGTTGGGGCCTCCAGGAAATC 244
              |||| |||||||||||| ||||| |||||||| || || ||  |||||||||||||| |
Db       1173 CAGGTCAAGGGCTCAGGGGCTTGCAGGGCCCTCCAGGGAAACTGGGGCCTCCAGGAAGTG 1232

Qy        245 CAGGGCCTTCTGGGTCACCAGGACCAAAGGGCCAAAAAGGAGACCCTGGAAAAAG 299
              |||  |  ||||    | ||||||||| |||||||||| || | |||| | ||
Db       1233 TAGGAGCCCCTGGAAGTCAAGGACCAAAAGGCCAAAAAGGGGATCGTGGAGACAG 1287


RESULT 13
US-09-949-016-18342/c
; Sequence 18342, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 18342
;    LENGTH: 601
;    TYPE: DNA
;    ORGANISM: Human
US-09-949-016-18342

  Query Match              9.6%;  Score 72;  DB 4;  Length 601;
  Best Local Similarity   93.8%;  Pred. No. 1.7e-12;
  Matches   75;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy        295 AAAAGTCCGGATGGTGATAGTAGCCTGGCTGCCTCAGAAAGAAAAGCTCTGCAAACAGAA 354
              ||   ||  ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        129 AATTTTCTAGATGGTGATAGTAGCCTGGCTGCCTCAGAAAGAAAAGCTCTGCAAACAGAA 70

Qy        355 ATGGCACGTATCAAAAAGTG 374
              ||||||||||||||||||||
Db         69 ATGGCACGTATCAAAAAGTG 50


RESULT 14
US-09-949-016-124321/c
; Sequence 124321, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 124321
;    LENGTH: 601
;    TYPE: DNA
;    ORGANISM: Human
US-09-949-016-124321

  Query Match              9.6%;  Score 72;  DB 4;  Length 601;
  Best Local Similarity   93.8%;  Pred. No. 1.7e-12;
  Matches   75;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy        295 AAAAGTCCGGATGGTGATAGTAGCCTGGCTGCCTCAGAAAGAAAAGCTCTGCAAACAGAA 354
              ||   ||  ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        129 AATTTTCTAGATGGTGATAGTAGCCTGGCTGCCTCAGAAAGAAAAGCTCTGCAAACAGAA 70

Qy        355 ATGGCACGTATCAAAAAGTG 374
              ||||||||||||||||||||
Db         69 ATGGCACGTATCAAAAAGTG 50


RESULT 15
US-08-365-103B-3
; Sequence 3, Application US/08365103B
; Patent No. 5766943
;  GENERAL INFORMATION:
;    APPLICANT:  Lynch, Richard G
;    APPLICANT:  Nunez, Raphael D.
;    APPLICANT:  Yodoi, Jungi
;    TITLE OF INVENTION:  DNA Sequences for Soluble Froms of CD23
;    TITLE OF INVENTION:  and Methods of Use for Same
;    NUMBER OF SEQUENCES:  14
;    CORRESPONDENCE ADDRESS:
```

```
;       ADDRESSEE:  Zarley, McKee, Thomte, Voorhees & Sease
;       STREET:  801 Grand Ave. Suite 3200
;       CITY:  Des Moines
;       STATE:  Iowa
;       COUNTRY:  United States
;       ZIP:  50309
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.25
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/365,103B
;       FILING DATE:  28-DEC-1994
;       CLASSIFICATION:  435
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Nebel, Heidi S.
;       REGISTRATION NUMBER:  37,719
;       REFERENCE/DOCKET NUMBER:  Uirf N5-24
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (515) 288-3667
;       TELEFAX:  (515) 288-1338
;   INFORMATION FOR SEQ ID NO:  3:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  885 base pairs
;       TYPE:  nucleic acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  cDNA
;     HYPOTHETICAL:  NO
;     ANTI-SENSE:  NO
;     FEATURE:
;       NAME/KEY:  CDS
;       LOCATION:  24..884
US-08-365-103B-3

  Query Match             9.0%;  Score 67.6;  DB 1;  Length 885;
  Best Local Similarity   55.6%;  Pred. No. 5.5e-11;
  Matches  130;  Conservative    0;  Mismatches  104;  Indels    0;  Gaps    0;

Qy        484 GTGGCCACCCCCAGGAATGCTGCAGAGAATGGAGCCATTCAGAATCTCATCAAGGAGGAA 543
              ||   || || |||  |    | | || |       || ||  |  ||| |||| ||||
Db        567 GTCAGCATCCACAGCCAAAAGGAACAGGACTTCCTGATGCAACACATCAACAAGAAGGAT 626

Qy        544 GCCTTCCTGGGCATCACTGATGAGAAGACAGAAGGGCAGTTTGTGGATCTGACAGGAAAT 603
               |||   | ||| ||   |||   || |  || ||  |||||||       |   || |
Db        627 TCCTGGATTGGCCTCCAGGATCTCAATATGGAGGGAGAGTTTGTATGGTCGGACGGGAGC 686

Qy        604 AGACTGACCTACACAAACTGGAACGAGGGTGAACCCAACAATGCTGGTTCTGATGAAGAT 663
              ||   || |  ||||||||    || || ||||| || |  ||    | ||| ||
Db        687 CCTGTGGGTTATAGCAACTGGAATCCAGGGGAGCCCAATAACGGGGGCCAGGGTGAGGAC 746

Qy        664 TGTGTATTGCTACTGAAAAATGGCCAGTGGAATGACGTCCCCTGCTCCACCTCC 717
              |||||  || | | |  |   |||||||||||| |||| |  ||||  || || |
Db        747 TGTGTGATGATGCGGGGATCCGGCCAGTGGAACGACGCCTTCTGCCGCAGCTAC 800

Search completed: June 20, 2005, 17:05:13
Job time : 185 secs
```

THIS PAGE BLANK (USPTO)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 20, 2005, 16:02:01 ; Search time 1644 Seconds
(without alignments)
2820.582 Million cell updates/sec

Title: US-10-054-536-2
Perfect score: 747
Sequence: 1 atgtccctgtttccatcact.....tctgtgagttccctatctga 747

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 6054689 seqs, 3103772919 residues

Total number of hits satisfying chosen parameters: 12109378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_NA:*
1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
6: /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq:*
7: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
8: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
9: /cgn2_6/ptodata/2/pubpna/US09A_PUBCOMB.seq:*
10: /cgn2_6/ptodata/2/pubpna/US09B_PUBCOMB.seq:*
11: /cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq:*
12: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
13: /cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
14: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
15: /cgn2_6/ptodata/2/pubpna/US10C_PUBCOMB.seq:*
16: /cgn2_6/ptodata/2/pubpna/US10D_PUBCOMB.seq:*
17: /cgn2_6/ptodata/2/pubpna/US10E_PUBCOMB.seq:*
18: /cgn2_6/ptodata/2/pubpna/US10F_PUBCOMB.seq:*
19: /cgn2_6/ptodata/2/pubpna/US10G_PUBCOMB.seq:*
20: /cgn2_6/ptodata/2/pubpna/US10H_PUBCOMB.seq:*
21: /cgn2_6/ptodata/2/pubpna/US10I_PUBCOMB.seq:*
22: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
23: /cgn2_6/ptodata/2/pubpna/US11A_PUBCOMB.seq:*
24: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq:*
25: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
26: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	747	100.0	747	16	US-10-054-536-2	Sequence 2, Appli
2	747	100.0	747	22	US-10-500-774-2	Sequence 2, Appli
3	747	100.0	3605	9	US-09-880-107-3705	Sequence 3705, Ap
4	747	100.0	3605	16	US-10-054-536-1	Sequence 1, Appli
5	747	100.0	3605	17	US-10-429-160-57	Sequence 57, Appl
6	747	100.0	3605	22	US-10-500-774-1	Sequence 1, Appli
7	741.2	99.2	2159	21	US-10-844-837-99	Sequence 99, Appl
8	684	91.6	684	9	US-09-971-475-2	Sequence 2, Appli
9	444.6	59.5	1409	14	US-10-076-816-54	Sequence 54, Appl
10	373.2	50.0	1069	21	US-10-764-420-2521	Sequence 2521, Ap
11	364.6	48.8	1037	9	US-09-917-800A-1710	Sequence 1710, Ap
12	287.6	38.5	1068	17	US-10-388-934-107	Sequence 107, App
13	222	29.7	419	9	US-09-960-352-11785	Sequence 11785, A
14	186.2	24.9	405	19	US-10-450-472-58	Sequence 58, Appl
15	186	24.9	1802	18	US-10-070-415A-45	Sequence 45, Appl
16	186	24.9	1802	18	US-10-070-415A-49	Sequence 49, Appl
17	186	24.9	1802	18	US-10-070-415A-53	Sequence 53, Appl
c 18	185.6	24.8	463	19	US-10-469-285-750	Sequence 750, App
19	185	24.8	1802	18	US-10-070-415A-41	Sequence 41, Appl
20	185	24.8	1802	18	US-10-070-415A-42	Sequence 42, Appl
21	185	24.8	1802	18	US-10-070-415A-43	Sequence 43, Appl
22	185	24.8	1802	18	US-10-070-415A-44	Sequence 44, Appl
23	184.4	24.7	1802	18	US-10-070-415A-46	Sequence 46, Appl
24	184.4	24.7	1802	18	US-10-070-415A-47	Sequence 47, Appl
25	184.4	24.7	1802	18	US-10-070-415A-48	Sequence 48, Appl
26	184.4	24.7	1802	18	US-10-070-415A-50	Sequence 50, Appl
27	184.4	24.7	1802	18	US-10-070-415A-51	Sequence 51, Appl
28	184.4	24.7	1802	18	US-10-070-415A-52	Sequence 52, Appl
29	184.4	24.7	1802	18	US-10-070-415A-54	Sequence 54, Appl
30	184.4	24.7	1802	18	US-10-070-415A-55	Sequence 55, Appl
31	184.4	24.7	1802	18	US-10-070-415A-56	Sequence 56, Appl
32	131.6	17.6	351	9	US-09-960-352-10110	Sequence 10110, A
c 33	112.4	15.0	5815	15	US-10-311-455-1208	Sequence 1208, Ap
34	108	14.5	542	17	US-10-388-934-108	Sequence 108, App
35	108	14.5	5815	15	US-10-311-455-1207	Sequence 1207, Ap
36	107.2	14.4	240	9	US-09-960-352-14616	Sequence 14616, A
37	100	13.4	140	11	US-09-727-030C-1	Sequence 1, Appli
38	95.6	12.8	221	9	US-09-960-352-2772	Sequence 2772, Ap
39	94.6	12.7	1128	20	US-10-830-959-3	Sequence 3, Appli
40	94.6	12.7	1313	14	US-10-116-802-47	Sequence 47, Appl
41	94.6	12.7	1410	9	US-09-954-456-2274	Sequence 2274, Ap
42	94.6	12.7	1410	21	US-10-843-641A-5301	Sequence 5301, Ap
43	94.6	12.7	2540	21	US-10-844-837-100	Sequence 100, App
44	93.6	12.5	408	19	US-10-450-472-60	Sequence 60, Appl
45	92.6	12.4	534	20	US-10-830-959-2	Sequence 2, Appli

ALIGNMENTS

RESULT 1
US-10-054-536-2
; Sequence 2, Application US/10054536
; Publication No. US20030162248A1
; GENERAL INFORMATION:
; APPLICANT: Wakamiya, No. US20030162248A1utaka
; TITLE OF INVENTION: RECOMBINANT HUMAN MANNAN-BINDING PROTEINS AND PROCESS
; TITLE OF INVENTION: FOR PRODUCING THE SAME
; FILE REFERENCE: 19036/36614
; CURRENT APPLICATION NUMBER: US/10/054,536
; CURRENT FILING DATE: 2002-01-22
; PRIOR APPLICATION NUMBER: PCT/JP98/03311
; PRIOR FILING DATE: 1998-07-23
; PRIOR APPLICATION NUMBER: JP 10-11864
; PRIOR FILING DATE: 1998-01-23
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 747
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-054-536-2

Query Match 100.0%; Score 747; DB 16; Length 747;
Best Local Similarity 100.0%; Pred. No. 2.9e-234;
Matches 747; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 ATGTCCCTGTTTCCATCACTCCCTCTCCTTCTCCTGAGTATGGTGGCAGCGTCTTACTCA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGTCCCTGTTTCCATCACTCCCTCTCCTTCTCCTGAGTATGGTGGCAGCGTCTTACTCA 60
```

```
Qy        61 GAAACTGTGACCTGTGAGGATGCCCAAAAGACCTGCCCTGCAGTGATTGCCTGTAGCTCT 120
Db        61 GAAACTGTGACCTGTGAGGATGCCCAAAAGACCTGCCCTGCAGTGATTGCCTGTAGCTCT 120

Qy       121 CCAGGCATCAACGGCTTCCCAGGCAAAGATGGGCGTGATGGCACCAAGGGAGAAAAGGGG 180
Db       121 CCAGGCATCAACGGCTTCCCAGGCAAAGATGGGCGTGATGGCACCAAGGGAGAAAAGGGG 180

Qy       181 GAACCAGGCCAAGGGCTCAGAGGCTTACAGGGCCCCCCTGGAAAGTTGGGGCCTCCAGGA 240
Db       181 GAACCAGGCCAAGGGCTCAGAGGCTTACAGGGCCCCCCTGGAAAGTTGGGGCCTCCAGGA 240

Qy       241 AATCCAGGGCCTTCTGGGTCACCAGGACCAAAGGGCCAAAAAGGAGACCCTGGAAAAAGT 300
Db       241 AATCCAGGGCCTTCTGGGTCACCAGGACCAAAGGGCCAAAAAGGAGACCCTGGAAAAAGT 300

Qy       301 CCGGATGGTGATAGTAGCCTGGCTGCCTCAGAAAGAAAAGCTCTGCAAACAGAAATGGCA 360
Db       301 CCGGATGGTGATAGTAGCCTGGCTGCCTCAGAAAGAAAAGCTCTGCAAACAGAAATGGCA 360

Qy       361 CGTATCAAAAAGTGGCTGACCTTCTCTCTGGGCAAACAAGTTGGGAACAAGTTCTTCCTG 420
Db       361 CGTATCAAAAAGTGGCTGACCTTCTCTCTGGGCAAACAAGTTGGGAACAAGTTCTTCCTG 420

Qy       421 ACCAATGGTGAAATAATGACCTTTGAAAAAGTGAAGGCCTTGTGTGTCAAGTTCCAGGCC 480
Db       421 ACCAATGGTGAAATAATGACCTTTGAAAAAGTGAAGGCCTTGTGTGTCAAGTTCCAGGCC 480

Qy       481 TCTGTGGCCACCCCCAGGAATGCTGCAGAGAATGGAGCCATTCAGAATCTCATCAAGGAG 540
Db       481 TCTGTGGCCACCCCCAGGAATGCTGCAGAGAATGGAGCCATTCAGAATCTCATCAAGGAG 540

Qy       541 GAAGCCTTCCTGGGCATCACTGATGAGAAGACAGAAGGGCAGTTTGTGGATCTGACAGGA 600
Db       541 GAAGCCTTCCTGGGCATCACTGATGAGAAGACAGAAGGGCAGTTTGTGGATCTGACAGGA 600

Qy       601 AATAGACTGACCTACACAAACTGGAACGAGGGTGAACCCAACAATGCTGGTTCTGATGAA 660
Db       601 AATAGACTGACCTACACAAACTGGAACGAGGGTGAACCCAACAATGCTGGTTCTGATGAA 660

Qy       661 GATTGTGTATTGCTACTGAAAAATGGCCAGTGGAATGACGTCCCCTGCTCCACCTCCCAT 720
Db       661 GATTGTGTATTGCTACTGAAAAATGGCCAGTGGAATGACGTCCCCTGCTCCACCTCCCAT 720

Qy       721 CTGGCCGTCTGTGAGTTCCCTATCTGA 747
Db       721 CTGGCCGTCTGTGAGTTCCCTATCTGA 747
```

RESULT 2
US-10-500-774-2
; Sequence 2, Application US/10500774
; Publication No. US20050123899A1
; GENERAL INFORMATION:
; APPLICANT: FUSO PHARMACEUTICAL INDUSTRIES, LTD.
; TITLE OF INVENTION: Anti-HIV Agent
; FILE REFERENCE: 03P451WO
; CURRENT APPLICATION NUMBER: US/10/500,774
; CURRENT FILING DATE: 2004-07-06
; PRIOR APPLICATION NUMBER: JP 2002-189534
; PRIOR FILING DATE: 2002-06-28
; NUMBER OF SEQ ID NOS: 3
; SEQ ID NO 2
; LENGTH: 747
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-500-774-2

Query Match 100.0%; Score 747; DB 22; Length 747;
Best Local Similarity 100.0%; Pred. No. 2.9e-234;
Matches 747; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy         1 ATGTCCCTGTTTCCATCACTCCCTCTCCTTCTCCTGAGTATGGTGGCAGCGTCTTACTCA 60
Db         1 ATGTCCCTGTTTCCATCACTCCCTCTCCTTCTCCTGAGTATGGTGGCAGCGTCTTACTCA 60

Qy        61 GAAACTGTGACCTGTGAGGATGCCCAAAAGACCTGCCCTGCAGTGATTGCCTGTAGCTCT 120
Db        61 GAAACTGTGACCTGTGAGGATGCCCAAAAGACCTGCCCTGCAGTGATTGCCTGTAGCTCT 120

Qy       121 CCAGGCATCAACGGCTTCCCAGGCAAAGATGGGCGTGATGGCACCAAGGGAGAAAAGGGG 180
Db       121 CCAGGCATCAACGGCTTCCCAGGCAAAGATGGGCGTGATGGCACCAAGGGAGAAAAGGGG 180

Qy       181 GAACCAGGCCAAGGGCTCAGAGGCTTACAGGGCCCCCCTGGAAAGTTGGGGCCTCCAGGA 240
Db       181 GAACCAGGCCAAGGGCTCAGAGGCTTACAGGGCCCCCCTGGAAAGTTGGGGCCTCCAGGA 240

Qy       241 AATCCAGGGCCTTCTGGGTCACCAGGACCAAAGGGCCAAAAAGGAGACCCTGGAAAAAGT 300
Db       241 AATCCAGGGCCTTCTGGGTCACCAGGACCAAAGGGCCAAAAAGGAGACCCTGGAAAAAGT 300

Qy       301 CCGGATGGTGATAGTAGCCTGGCTGCCTCAGAAAGAAAAGCTCTGCAAACAGAAATGGCA 360
Db       301 CCGGATGGTGATAGTAGCCTGGCTGCCTCAGAAAGAAAAGCTCTGCAAACAGAAATGGCA 360

Qy       361 CGTATCAAAAAGTGGCTGACCTTCTCTCTGGGCAAACAAGTTGGGAACAAGTTCTTCCTG 420
Db       361 CGTATCAAAAAGTGGCTGACCTTCTCTCTGGGCAAACAAGTTGGGAACAAGTTCTTCCTG 420

Qy       421 ACCAATGGTGAAATAATGACCTTTGAAAAAGTGAAGGCCTTGTGTGTCAAGTTCCAGGCC 480
Db       421 ACCAATGGTGAAATAATGACCTTTGAAAAAGTGAAGGCCTTGTGTGTCAAGTTCCAGGCC 480

Qy       481 TCTGTGGCCACCCCCAGGAATGCTGCAGAGAATGGAGCCATTCAGAATCTCATCAAGGAG 540
Db       481 TCTGTGGCCACCCCCAGGAATGCTGCAGAGAATGGAGCCATTCAGAATCTCATCAAGGAG 540

Qy       541 GAAGCCTTCCTGGGCATCACTGATGAGAAGACAGAAGGGCAGTTTGTGGATCTGACAGGA 600
Db       541 GAAGCCTTCCTGGGCATCACTGATGAGAAGACAGAAGGGCAGTTTGTGGATCTGACAGGA 600

Qy       601 AATAGACTGACCTACACAAACTGGAACGAGGGTGAACCCAACAATGCTGGTTCTGATGAA 660
Db       601 AATAGACTGACCTACACAAACTGGAACGAGGGTGAACCCAACAATGCTGGTTCTGATGAA 660

Qy       661 GATTGTGTATTGCTACTGAAAAATGGCCAGTGGAATGACGTCCCCTGCTCCACCTCCCAT 720
Db       661 GATTGTGTATTGCTACTGAAAAATGGCCAGTGGAATGACGTCCCCTGCTCCACCTCCCAT 720

Qy       721 CTGGCCGTCTGTGAGTTCCCTATCTGA 747
Db       721 CTGGCCGTCTGTGAGTTCCCTATCTGA 747
```

RESULT 3
US-09-880-107-3705
; Sequence 3705, Application US/09880107
; Patent No. US20020142981A1
; GENERAL INFORMATION:
; APPLICANT: Horne, Darci T.
; APPLICANT: Vockley, Joseph G.
; APPLICANT: Scherf, Uwe
; APPLICANT: Gene Logic, Inc.
; TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer
; FILE REFERENCE: 44921-5028-WO
; CURRENT APPLICATION NUMBER: US/09/880,107
; CURRENT FILING DATE: 2001-06-14
; PRIOR APPLICATION NUMBER: US 60/211,379
; PRIOR FILING DATE: 2000-06-14
; PRIOR APPLICATION NUMBER: US 60/237,054
; PRIOR FILING DATE: 2000-10-02
; NUMBER OF SEQ ID NOS: 3950
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3705

```
;   LENGTH: 3605
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   OTHER INFORMATION: Genbank Accession No. US20020142981A1 X15422
US-09-880-107-3705

  Query Match             100.0%;  Score 747;  DB 9;  Length 3605;
  Best Local Similarity   100.0%;  Pred. No. 6e-234;
  Matches  747;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATGTCCCTGTTTCCATCACTCCCTCTCCTTCTCCTGAGTATGGTGGCAGCGTCTTACTCA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         66 ATGTCCCTGTTTCCATCACTCCCTCTCCTTCTCCTGAGTATGGTGGCAGCGTCTTACTCA 125

Qy         61 GAAACTGTGACCTGTGAGGATGCCCAAAAGACCTGCCCTGCAGTGATTGCCTGTAGCTCT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        126 GAAACTGTGACCTGTGAGGATGCCCAAAAGACCTGCCCTGCAGTGATTGCCTGTAGCTCT 185

Qy        121 CCAGGCATCAACGGCTTCCCAGGCAAAGATGGGCGTGATGGCACCAAGGGAGAAAAGGGG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        186 CCAGGCATCAACGGCTTCCCAGGCAAAGATGGGCGTGATGGCACCAAGGGAGAAAAGGGG 245

Qy        181 GAACCAGGCCAAGGGCTCAGAGGCTTACAGGGCCCCCCTGGAAAGTTGGGGCCTCCAGGA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        246 GAACCAGGCCAAGGGCTCAGAGGCTTACAGGGCCCCCCTGGAAAGTTGGGGCCTCCAGGA 305

Qy        241 AATCCAGGGCCTTCTGGGTCACCAGGACCAAAGGGCCAAAAAGGAGACCCTGGAAAAAGT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        306 AATCCAGGGCCTTCTGGGTCACCAGGACCAAAGGGCCAAAAAGGAGACCCTGGAAAAAGT 365

Qy        301 CCGGATGGTGATAGTAGCCTGGCTGCCTCAGAAAGAAAAGCTCTGCAAACAGAAATGGCA 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        366 CCGGATGGTGATAGTAGCCTGGCTGCCTCAGAAAGAAAAGCTCTGCAAACAGAAATGGCA 425

Qy        361 CGTATCAAAAAGTGGCTGACCTTCTCTCTGGGCAAACAAGTTGGGAACAAGTTCTTCCTG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        426 CGTATCAAAAAGTGGCTGACCTTCTCTCTGGGCAAACAAGTTGGGAACAAGTTCTTCCTG 485

Qy        421 ACCAATGGTGAAATAATGACCTTTGAAAAAGTGAAGGCCTTGTGTGTCAAGTTCCAGGCC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        486 ACCAATGGTGAAATAATGACCTTTGAAAAAGTGAAGGCCTTGTGTGTCAAGTTCCAGGCC 545

Qy        481 TCTGTGGCCACCCCCAGGAATGCTGCAGAGAATGGAGCCATTCAGAATCTCATCAAGGAG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        546 TCTGTGGCCACCCCCAGGAATGCTGCAGAGAATGGAGCCATTCAGAATCTCATCAAGGAG 605

Qy        541 GAAGCCTTCCTGGGCATCACTGATGAGAAGACAGAAGGGCAGTTTGTGGATCTGACAGGA 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        606 GAAGCCTTCCTGGGCATCACTGATGAGAAGACAGAAGGGCAGTTTGTGGATCTGACAGGA 665

Qy        601 AATAGACTGACCTACACAAACTGGAACGAGGGTGAACCCAACAATGCTGGTTCTGATGAA 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        666 AATAGACTGACCTACACAAACTGGAACGAGGGTGAACCCAACAATGCTGGTTCTGATGAA 725

Qy        661 GATTGTGTATTGCTACTGAAAAATGGCCAGTGGAATGACGTCCCCTGCTCCACCTCCCAT 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        726 GATTGTGTATTGCTACTGAAAAATGGCCAGTGGAATGACGTCCCCTGCTCCACCTCCCAT 785

Qy        721 CTGGCCGTCTGTGAGTTCCCTATCTGA 747
              |||||||||||||||||||||||||||
Db        786 CTGGCCGTCTGTGAGTTCCCTATCTGA 812


RESULT 4
US-10-054-536-1
; Sequence 1, Application US/10054536
; Publication No. US20030162248A1
; GENERAL INFORMATION:
;  APPLICANT: Wakamiya, No. US20030162248A1utaka
;  TITLE OF INVENTION: RECOMBINANT HUMAN MANNAN-BINDING PROTEINS AND PROCESS
;  TITLE OF INVENTION:  FOR PRODUCING THE SAME
;  FILE REFERENCE: 19036/36614
;  CURRENT APPLICATION NUMBER: US/10/054,536
;  CURRENT FILING DATE:  2002-01-22
;  PRIOR APPLICATION NUMBER: PCT/JP98/03311
;  PRIOR FILING DATE: 1998-07-23
;  PRIOR APPLICATION NUMBER: JP 10-11864
;  PRIOR FILING DATE: 1998-01-23
;  NUMBER OF SEQ ID NOS: 28
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
;   LENGTH: 3605
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (66)..(809)
;   FEATURE:
;   NAME/KEY: mat_peptide
;   LOCATION: (126)..(809)
US-10-054-536-1

  Query Match             100.0%;  Score 747;  DB 16;  Length 3605;
  Best Local Similarity   100.0%;  Pred. No. 6e-234;
  Matches  747;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATGTCCCTGTTTCCATCACTCCCTCTCCTTCTCCTGAGTATGGTGGCAGCGTCTTACTCA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         66 ATGTCCCTGTTTCCATCACTCCCTCTCCTTCTCCTGAGTATGGTGGCAGCGTCTTACTCA 125

Qy         61 GAAACTGTGACCTGTGAGGATGCCCAAAAGACCTGCCCTGCAGTGATTGCCTGTAGCTCT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        126 GAAACTGTGACCTGTGAGGATGCCCAAAAGACCTGCCCTGCAGTGATTGCCTGTAGCTCT 185

Qy        121 CCAGGCATCAACGGCTTCCCAGGCAAAGATGGGCGTGATGGCACCAAGGGAGAAAAGGGG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        186 CCAGGCATCAACGGCTTCCCAGGCAAAGATGGGCGTGATGGCACCAAGGGAGAAAAGGGG 245

Qy        181 GAACCAGGCCAAGGGCTCAGAGGCTTACAGGGCCCCCCTGGAAAGTTGGGGCCTCCAGGA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        246 GAACCAGGCCAAGGGCTCAGAGGCTTACAGGGCCCCCCTGGAAAGTTGGGGCCTCCAGGA 305

Qy        241 AATCCAGGGCCTTCTGGGTCACCAGGACCAAAGGGCCAAAAAGGAGACCCTGGAAAAAGT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        306 AATCCAGGGCCTTCTGGGTCACCAGGACCAAAGGGCCAAAAAGGAGACCCTGGAAAAAGT 365

Qy        301 CCGGATGGTGATAGTAGCCTGGCTGCCTCAGAAAGAAAAGCTCTGCAAACAGAAATGGCA 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        366 CCGGATGGTGATAGTAGCCTGGCTGCCTCAGAAAGAAAAGCTCTGCAAACAGAAATGGCA 425

Qy        361 CGTATCAAAAAGTGGCTGACCTTCTCTCTGGGCAAACAAGTTGGGAACAAGTTCTTCCTG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        426 CGTATCAAAAAGTGGCTGACCTTCTCTCTGGGCAAACAAGTTGGGAACAAGTTCTTCCTG 485

Qy        421 ACCAATGGTGAAATAATGACCTTTGAAAAAGTGAAGGCCTTGTGTGTCAAGTTCCAGGCC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        486 ACCAATGGTGAAATAATGACCTTTGAAAAAGTGAAGGCCTTGTGTGTCAAGTTCCAGGCC 545

Qy        481 TCTGTGGCCACCCCCAGGAATGCTGCAGAGAATGGAGCCATTCAGAATCTCATCAAGGAG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        546 TCTGTGGCCACCCCCAGGAATGCTGCAGAGAATGGAGCCATTCAGAATCTCATCAAGGAG 605

Qy        541 GAAGCCTTCCTGGGCATCACTGATGAGAAGACAGAAGGGCAGTTTGTGGATCTGACAGGA 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        606 GAAGCCTTCCTGGGCATCACTGATGAGAAGACAGAAGGGCAGTTTGTGGATCTGACAGGA 665

Qy        601 AATAGACTGACCTACACAAACTGGAACGAGGGTGAACCCAACAATGCTGGTTCTGATGAA 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        666 AATAGACTGACCTACACAAACTGGAACGAGGGTGAACCCAACAATGCTGGTTCTGATGAA 725

Qy        661 GATTGTGTATTGCTACTGAAAAATGGCCAGTGGAATGACGTCCCCTGCTCCACCTCCCAT 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        726 GATTGTGTATTGCTACTGAAAAATGGCCAGTGGAATGACGTCCCCTGCTCCACCTCCCAT 785

Qy        721 CTGGCCGTCTGTGAGTTCCCTATCTGA 747
```

```
                    ||||||||||||||||||||||||||
Db        786 CTGGCCGTCTGTGAGTTCCCTATCTGA 812


RESULT 5
US-10-429-160-57
; Sequence 57, Application US/10429160
; Publication No. US20040023276A1
; GENERAL INFORMATION:
;  APPLICANT: Ward, Teresa R
;  APPLICANT:  Mao, Mao
;  APPLICANT:  Linsley, Peter S
;  APPLICANT:  Lund, Lund
;  TITLE OF INVENTION: LXR Ligand Induced Genes and Proteins
;  FILE REFERENCE: RS0200
;  CURRENT APPLICATION NUMBER: US/10/429,160
;  CURRENT FILING DATE:  2003-05-02
;  PRIOR APPLICATION NUMBER: US 60/377,714
;  PRIOR FILING DATE: 2002-05-03
;  NUMBER OF SEQ ID NOS: 111
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 57
;   LENGTH: 3605
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-429-160-57

  Query Match           100.0%;  Score 747;  DB 17;  Length 3605;
  Best Local Similarity  100.0%;  Pred. No. 6e-234;
  Matches  747;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATGTCCCTGTTTCCATCACTCCCTCTCCTTCTCCTGAGTATGGTGGCAGCGTCTTACTCA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         66 ATGTCCCTGTTTCCATCACTCCCTCTCCTTCTCCTGAGTATGGTGGCAGCGTCTTACTCA 125

Qy         61 GAAACTGTGACCTGTGAGGATGCCCAAAAGACCTGCCCTGCAGTGATTGCCTGTAGCTCT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        126 GAAACTGTGACCTGTGAGGATGCCCAAAAGACCTGCCCTGCAGTGATTGCCTGTAGCTCT 185

Qy        121 CCAGGCATCAACGGCTTCCCAGGCAAAGATGGGCGTGATGGCACCAAGGGAGAAAAGGGG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        186 CCAGGCATCAACGGCTTCCCAGGCAAAGATGGGCGTGATGGCACCAAGGGAGAAAAGGGG 245

Qy        181 GAACCAGGCCAAGGGCTCAGAGGCTTACAGGGCCCCCCTGGAAAGTTGGGGCCTCCAGGA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        246 GAACCAGGCCAAGGGCTCAGAGGCTTACAGGGCCCCCCTGGAAAGTTGGGGCCTCCAGGA 305

Qy        241 AATCCAGGGCCTTCTGGGTCACCAGGACCAAAGGGCCAAAAAGGAGACCCTGGAAAAAGT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        306 AATCCAGGGCCTTCTGGGTCACCAGGACCAAAGGGCCAAAAAGGAGACCCTGGAAAAAGT 365

Qy        301 CCGGATGGTGATAGTAGCCTGGCTGCCTCAGAAAGAAAAGCTCTGCAAACAGAAATGGCA 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        366 CCGGATGGTGATAGTAGCCTGGCTGCCTCAGAAAGAAAAGCTCTGCAAACAGAAATGGCA 425

Qy        361 CGTATCAAAAAGTGGCTGACCTTCTCTCTGGGCAAACAAGTTGGGAACAAGTTCTTCCTG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        426 CGTATCAAAAAGTGGCTGACCTTCTCTCTGGGCAAACAAGTTGGGAACAAGTTCTTCCTG 485

Qy        421 ACCAATGGTGAAATAATGACCTTTGAAAAAGTGAAGGCCTTGTGTGTCAAGTTCCAGGCC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        486 ACCAATGGTGAAATAATGACCTTTGAAAAAGTGAAGGCCTTGTGTGTCAAGTTCCAGGCC 545

Qy        481 TCTGTGGCCACCCCCAGGAATGCTGCAGAGAATGGAGCCATTCAGAATCTCATCAAGGAG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        546 TCTGTGGCCACCCCCAGGAATGCTGCAGAGAATGGAGCCATTCAGAATCTCATCAAGGAG 605

Qy        541 GAAGCCTTCCTGGGCATCACTGATGAGAAGACAGAAGGGCAGTTTGTGGATCTGACAGGA 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        606 GAAGCCTTCCTGGGCATCACTGATGAGAAGACAGAAGGGCAGTTTGTGGATCTGACAGGA 665

Qy        601 AATAGACTGACCTACACAAACTGGAACGAGGGTGAACCCAACAATGCTGGTTCTGATGAA 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        666 AATAGACTGACCTACACAAACTGGAACGAGGGTGAACCCAACAATGCTGGTTCTGATGAA 725

Qy        661 GATTGTGTATTGCTACTGAAAAATGGCCAGTGGAATGACGTCCCCTGCTCCACCTCCCAT 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        726 GATTGTGTATTGCTACTGAAAAATGGCCAGTGGAATGACGTCCCCTGCTCCACCTCCCAT 785

Qy        721 CTGGCCGTCTGTGAGTTCCCTATCTGA 747
              |||||||||||||||||||||||||||
Db        786 CTGGCCGTCTGTGAGTTCCCTATCTGA 812


RESULT 6
US-10-500-774-1
; Sequence 1, Application US/10500774
; Publication No. US20050123899A1
; GENERAL INFORMATION:
;  APPLICANT: FUSO PHARMACEUTICAL INDUSTRIES, LTD.
;  TITLE OF INVENTION: Anti-HIV Agent
;  FILE REFERENCE: 03P451WO
;  CURRENT APPLICATION NUMBER: US/10/500,774
;  CURRENT FILING DATE:  2004-07-06
;  PRIOR APPLICATION NUMBER: JP 2002-189534
;  PRIOR FILING DATE: 2002-06-28
;  NUMBER OF SEQ ID NOS: 3
; SEQ ID NO 1
;   LENGTH: 3605
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-500-774-1

  Query Match           100.0%;  Score 747;  DB 22;  Length 3605;
  Best Local Similarity  100.0%;  Pred. No. 6e-234;
  Matches  747;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATGTCCCTGTTTCCATCACTCCCTCTCCTTCTCCTGAGTATGGTGGCAGCGTCTTACTCA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         66 ATGTCCCTGTTTCCATCACTCCCTCTCCTTCTCCTGAGTATGGTGGCAGCGTCTTACTCA 125

Qy         61 GAAACTGTGACCTGTGAGGATGCCCAAAAGACCTGCCCTGCAGTGATTGCCTGTAGCTCT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        126 GAAACTGTGACCTGTGAGGATGCCCAAAAGACCTGCCCTGCAGTGATTGCCTGTAGCTCT 185

Qy        121 CCAGGCATCAACGGCTTCCCAGGCAAAGATGGGCGTGATGGCACCAAGGGAGAAAAGGGG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        186 CCAGGCATCAACGGCTTCCCAGGCAAAGATGGGCGTGATGGCACCAAGGGAGAAAAGGGG 245

Qy        181 GAACCAGGCCAAGGGCTCAGAGGCTTACAGGGCCCCCCTGGAAAGTTGGGGCCTCCAGGA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        246 GAACCAGGCCAAGGGCTCAGAGGCTTACAGGGCCCCCCTGGAAAGTTGGGGCCTCCAGGA 305

Qy        241 AATCCAGGGCCTTCTGGGTCACCAGGACCAAAGGGCCAAAAAGGAGACCCTGGAAAAAGT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        306 AATCCAGGGCCTTCTGGGTCACCAGGACCAAAGGGCCAAAAAGGAGACCCTGGAAAAAGT 365

Qy        301 CCGGATGGTGATAGTAGCCTGGCTGCCTCAGAAAGAAAAGCTCTGCAAACAGAAATGGCA 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        366 CCGGATGGTGATAGTAGCCTGGCTGCCTCAGAAAGAAAAGCTCTGCAAACAGAAATGGCA 425

Qy        361 CGTATCAAAAAGTGGCTGACCTTCTCTCTGGGCAAACAAGTTGGGAACAAGTTCTTCCTG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        426 CGTATCAAAAAGTGGCTGACCTTCTCTCTGGGCAAACAAGTTGGGAACAAGTTCTTCCTG 485

Qy        421 ACCAATGGTGAAATAATGACCTTTGAAAAAGTGAAGGCCTTGTGTGTCAAGTTCCAGGCC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        486 ACCAATGGTGAAATAATGACCTTTGAAAAAGTGAAGGCCTTGTGTGTCAAGTTCCAGGCC 545

Qy        481 TCTGTGGCCACCCCCAGGAATGCTGCAGAGAATGGAGCCATTCAGAATCTCATCAAGGAG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        546 TCTGTGGCCACCCCCAGGAATGCTGCAGAGAATGGAGCCATTCAGAATCTCATCAAGGAG 605

Qy        541 GAAGCCTTCCTGGGCATCACTGATGAGAAGACAGAAGGGCAGTTTGTGGATCTGACAGGA 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        606 GAAGCCTTCCTGGGCATCACTGATGAGAAGACAGAAGGGCAGTTTGTGGATCTGACAGGA 665
```

```
Qy        601 AATAGACTGACCTACACAAACTGGAACGAGGGTGAACCCAACAATGCTGGTTCTGATGAA 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        666 AATAGACTGACCTACACAAACTGGAACGAGGGTGAACCCAACAATGCTGGTTCTGATGAA 725

Qy        661 GATTGTGTATTGCTACTGAAAAATGGCCAGTGGAATGACGTCCCCTGCTCCACCTCCCAT 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        726 GATTGTGTATTGCTACTGAAAAATGGCCAGTGGAATGACGTCCCCTGCTCCACCTCCCAT 785

Qy        721 CTGGCCGTCTGTGAGTTCCCTATCTGA 747
              |||||||||||||||||||||||||||
Db        786 CTGGCCGTCTGTGAGTTCCCTATCTGA 812


RESULT 7
US-10-844-837-99
; Sequence 99, Application US/10844837
; Publication No. US20050014932A1
; GENERAL INFORMATION:
;  APPLICANT: Imboden, Michael
;  APPLICANT:  Homan, Jane
;  APPLICANT:  Bremel, Robert D.
;  TITLE OF INVENTION: Targeted Biocides
;  FILE REFERENCE: IOGEN-09014
;  CURRENT APPLICATION NUMBER: US/10/844,837
;  CURRENT FILING DATE:  2004-05-13
;  NUMBER OF SEQ ID NOS: 101
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 99
;   LENGTH: 2159
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-844-837-99

  Query Match             99.2%;  Score 741.2;  DB 21;  Length 2159;
  Best Local Similarity   99.6%;  Pred. No. 3.8e-232;
  Matches  743;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 ATGTCCCTGTTTCCATCACTCCCTCTCCTTCTCCTGAGTATGGTGGCAGCGTCTTACTCA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        679 ATGTCCCTGTTTCCATCACTCCCTCTCCTTCTCCTGAGTATGGTGGCAGCGTCTTACTCA 738

Qy         61 GAAACTGTGACCTGTGAGGATGCCCAAAAGACCTGCCCTGCAGTGATTGCCTGTAGCTCT 120
              |||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        739 GAAACTGTGGCCTGTGAGGATGCCCAAAAGACCTGCCCTGCAGTGATTGCCTGTAGCTCT 798

Qy        121 CCAGGCATCAACGGCTTCCCAGGCAAAGATGGGCGTGATGGCACCAAGGGAGAAAAGGGG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        799 CCAGGCATCAACGGCTTCCCAGGCAAAGATGGGCGTGATGGCACCAAGGGAGAAAAGGGG 858

Qy        181 GAACCAGGCCAAGGGCTCAGAGGCTTACAGGGCCCCCCTGGAAAGTTGGGGCCTCCAGGA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        859 GAACCAGGCCAAGGGCTCAGAGGCTTACAGGGCCCCCCTGGAAAGTTGGGGCCTCCAGGA 918

Qy        241 AATCCAGGGCCTTCTGGGTCACCAGGACCAAAGGGCCAAAAAGGAGACCCTGGAAAAAGT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        919 AATCCAGGGCCTTCTGGGTCACCAGGACCAAAGGGCCAAAAAGGAGACCCTGGAAAAAGT 978

Qy        301 CCGGATGGTGATAGTAGCCTGGCTGCCTCAGAAAGAAAAGCTCTGCAAACAGAAATGGCA 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        979 CCGGATGGTGATAGTAGCCTGGCTGCCTCAGAAAGAAAAGCTCTGCAAACAGAAATGGCA 1038

Qy        361 CGTATCAAAAAGTGGCTGACCTTCTCTCTGGGCAAACAAGTTGGGAACAAGTTCTTCCTG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1039 CGTATCAAAAAGTGGCTGACCTTCTCTCTGGGCAAACAAGTTGGGAACAAGTTCTTCCTG 1098

Qy        421 ACCAATGGTGAAATAATGACCTTTGAAAAAGTGAAGGCCTTGTGTGTCAAGTTCCAGGCC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1099 ACCAATGGTGAAATAATGACCTTTGAAAAAGTGAAGGCCTTGTGTGTCAAGTTCCAGGCC 1158

Qy        481 TCTGTGGCCACCCCCAGGAATGCTGCAGAGAATGGAGCCATTCAGAATCTCATCAAGGAG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1159 TCTGTGGCCACCCCCAGGAATGCTGCAGAGAATGGAGCCATTCAGAATCTCATCAAGGAG 1218

Qy        541 GAAGCCTTCCTGGGCATCACTGATGAGAAGACAGAAGGGCAGTTTGTGGATCTGACAGGA 600
              |||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Db       1219 GAAGCCTTCCTGGGTATCACTGATGAGAAGACAGAAGGGCAGTTTGTGGATCTGACAGGA 1278

Qy        601 AATAGACTGACCTACACAAACTGGAACGAGGGTGAACCCAACAATGCTGGTTCTGATGAA 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1279 AATAGACTGACCTACACAAACTGGAACGAGGGTGAACCCAACAATGCTGGTTCTGATGAA 1338

Qy        661 GATTGTGTATTGCTACTGAAAAATGGCCAGTGGAATGACGTCCCCTGCTCCACCTCCCAT 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1339 GATTGTGTATTGCTACTGAAAAATGGCCAGTGGAATGACGTCCCCTGCTCCACCTCCCAT 1398

Qy        721 CTGGCCGTCTGTGAGTTCCCTATCTG 746
              |||||||||||||||||||||||||| |
Db       1399 CTGGCCGTCTGTGAGTTCCCTATCGG 1424


RESULT 8
US-09-971-475-2
; Sequence 2, Application US/09971475
; Publication No. US20020086817A1
; GENERAL INFORMATION:
;  APPLICANT: Kawasaki, Toshisuke
;  TITLE OF INVENTION: Anticancer agent
;  FILE REFERENCE: ADT 308
;  CURRENT APPLICATION NUMBER: US/09/971,475
;  CURRENT FILING DATE:  2001-10-04
;  PRIOR APPLICATION NUMBER: US 09/468,705
;  PRIOR FILING DATE: 1999-12-21
;  PRIOR APPLICATION NUMBER: PCT/JP98/03697
;  PRIOR FILING DATE: 1998-08-19
;  PRIOR APPLICATION NUMBER: JP 239113/97
;  PRIOR FILING DATE: 1997-08-21
;  NUMBER OF SEQ ID NOS: 2
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
;   LENGTH: 684
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-971-475-2

  Query Match             91.6%;  Score 684;  DB 9;  Length 684;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-213;
  Matches  684;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         61 GAAACTGTGACCTGTGAGGATGCCCAAAAGACCTGCCCTGCAGTGATTGCCTGTAGCTCT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GAAACTGTGACCTGTGAGGATGCCCAAAAGACCTGCCCTGCAGTGATTGCCTGTAGCTCT 60

Qy        121 CCAGGCATCAACGGCTTCCCAGGCAAAGATGGGCGTGATGGCACCAAGGGAGAAAAGGGG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CCAGGCATCAACGGCTTCCCAGGCAAAGATGGGCGTGATGGCACCAAGGGAGAAAAGGGG 120

Qy        181 GAACCAGGCCAAGGGCTCAGAGGCTTACAGGGCCCCCCTGGAAAGTTGGGGCCTCCAGGA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GAACCAGGCCAAGGGCTCAGAGGCTTACAGGGCCCCCCTGGAAAGTTGGGGCCTCCAGGA 180

Qy        241 AATCCAGGGCCTTCTGGGTCACCAGGACCAAAGGGCCAAAAAGGAGACCCTGGAAAAAGT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 AATCCAGGGCCTTCTGGGTCACCAGGACCAAAGGGCCAAAAAGGAGACCCTGGAAAAAGT 240

Qy        301 CCGGATGGTGATAGTAGCCTGGCTGCCTCAGAAAGAAAAGCTCTGCAAACAGAAATGGCA 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CCGGATGGTGATAGTAGCCTGGCTGCCTCAGAAAGAAAAGCTCTGCAAACAGAAATGGCA 300

Qy        361 CGTATCAAAAAGTGGCTGACCTTCTCTCTGGGCAAACAAGTTGGGAACAAGTTCTTCCTG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 CGTATCAAAAAGTGGCTGACCTTCTCTCTGGGCAAACAAGTTGGGAACAAGTTCTTCCTG 360

Qy        421 ACCAATGGTGAAATAATGACCTTTGAAAAAGTGAAGGCCTTGTGTGTCAAGTTCCAGGCC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 ACCAATGGTGAAATAATGACCTTTGAAAAAGTGAAGGCCTTGTGTGTCAAGTTCCAGGCC 420
```

```
Qy        481 TCTGTGGCCACCCCCAGGAATGCTGCAGAGAATGGAGCCATTCAGAATCTCATCAAGGAG 540
Db        421 TCTGTGGCCACCCCCAGGAATGCTGCAGAGAATGGAGCCATTCAGAATCTCATCAAGGAG 480

Qy        541 GAAGCCTTCCTGGGCATCACTGATGAGAAGACAGAAGGGCAGTTTGTGGATCTGACAGGA 600
Db        481 GAAGCCTTCCTGGGCATCACTGATGAGAAGACAGAAGGGCAGTTTGTGGATCTGACAGGA 540

Qy        601 AATAGACTGACCTACACAAACTGGAACGAGGGTGAACCCAACAATGCTGGTTCTGATGAA 660
Db        541 AATAGACTGACCTACACAAACTGGAACGAGGGTGAACCCAACAATGCTGGTTCTGATGAA 600

Qy        661 GATTGTGTATTGCTACTGAAAAATGGCCAGTGGAATGACGTCCCCTGCTCCACCTCCCAT 720
Db        601 GATTGTGTATTGCTACTGAAAAATGGCCAGTGGAATGACGTCCCCTGCTCCACCTCCCAT 660

Qy        721 CTGGCCGTCTGTGAGTTCCCTATC 744
Db        661 CTGGCCGTCTGTGAGTTCCCTATC 684
```

RESULT 9
US-10-076-816-54
; Sequence 54, Application US/10076816
; Publication No. US20030056244A1
; GENERAL INFORMATION:
; APPLICANT: Huang, Ning
; APPLICANT: Rodrguez, Raymond
; APPLICANT: Hagie, Frank E.
; TITLE OF INVENTION: Feed Additive Compositions and Methods
; FILE REFERENCE: 50665-8021.US00
; CURRENT APPLICATION NUMBER: US/10/076,816
; CURRENT FILING DATE: 2002-02-14
; PRIOR APPLICATION NUMBER: US 60/269,188
; PRIOR FILING DATE: 2001-02-14
; PRIOR APPLICATION NUMBER: US 09/847,232
; PRIOR FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: US 60/266,929
; PRIOR FILING DATE: 2001-02-06
; PRIOR APPLICATION NUMBER: US 60/201,182
; PRIOR FILING DATE: 2000-05-02
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 54
; LENGTH: 1409
; TYPE: DNA
; ORGANISM: Bos taurus
US-10-076-816-54

Query Match 59.5%; Score 444.6; DB 14; Length 1409;
Best Local Similarity 76.4%; Pred. No. 8.1e-135;
Matches 575; Conservative 0; Mismatches 169; Indels 9; Gaps 2;

```
Qy          1 ATGTCCCTGTTTCCATCACTCCCTCTCCTTCTCCTGAGTATGGTGGCAGCGTCTT----- 55
Db         16 ATGTCGCTGTTTACATCACTTCCTTTTCTTCTCCTGACTGCGGTGACAGCATCTTGTGCA 75

Qy         56 -ACTCAGAAACTGTGACCTGTGAGGATGCCCAAAAGACCTGCCCTGCAGTGATTGCCTGT 114
Db         76 GACACAGAAACAGAGAACTGTGAGAACATCCGGAAGACCTGCC---CCGTGATTGCCTGT 132

Qy        115 AGCTCTCCAGGCATCAACGGCTTCCCAGGCAAAGATGGGCGTGATGGCACCAAGGGAGAA 174
Db        133 GGTCCTCCGGGCATCAATGGCATCCCAGGCAAAGATGGGCGTGATGGTGCCAAGGGAGAA 192

Qy        175 AAGGGGGAACCAGGCCAAGGGCTCAGAGGCTTACAGGGCCCCCCTGGAAAGTTGGGGCCT 234
Db        193 AAGGGAGAACCAGGTCAAGGACTCAGAGGCTCGCAGGGCCCCCCTGGAAAGATGGGGCCT 252

Qy        235 CCAGGAAATCCAGGGCCTTCTGGGTCACCAGGACCAAAGGGCCAAAAAGGAGACCCTGGA 294
Db        253 CAAGGAACGCCAGGGATCCCTGGGATACCAGGACCAATAGGCCAAAAAGGAGACCCTGGA 312

Qy        295 AAAAGTCCGGATGGTGATAGTAGCCTGGCTGCCTCAGAAAGAAAAGCTCTGCAAACAGAA 354
Db        313 GAAAATATGGGTGACTATATTCGCCTGGCTACTTCAGAAAGAGCAACTCTACAATCTGAA 372

Qy        355 ATGGCACGTATCAAAAAGTGGCTGACCTTCTCTCTGGGCAAACAAGTTGGGAACAAGTTC 414
Db        373 TTGAACCAGATCAAAAACTGGCTAATCTTCTCTCTGGGCAAAAGAGTTGGGAAGAAGGCA 432

Qy        415 TTCCTGACCAATGGTGAAATAATGACCTTTGAAAAAGTGAAGGCCTTGTGTGTCAAGTTC 474
Db        433 TTTTTTACCAATGGTAAAAAGATGCCTTTTAATGAAGTGAAGACTCTGTGTGCACAGTTC 492

Qy        475 CAGGCCTCTGTGGCCACCCCCAGGAATGCTGCAGAGAATGGAGCCATTCAGAATCTCATC 534
Db        493 CAGGGCCGTGTGGCCACCCCTATGAATGCTGAAGAAAACAGGGCCCTCAAGGATTTAGTC 552

Qy        535 AAGGAGGAAGCCTTCCTGGGCATCACTGATGAGAAGACAGAAGGGCAGTTTGTGGATCTG 594
Db        553 ACTGAAGAGGCCTTCCTGGGCATCACAGATCAGGAGACTGAAGGCAAATTTGTGGATCTG 612

Qy        595 ACAGGAAATAGACTGACCTACACAAACTGGAACGAGGGTGAACCCAACAATGCTGGTTCT 654
Db        613 ACAGGAAAGGGGGTGACCTACCAAAACTGGAATGATGGCGAGCCTAACAACGCTTCTCCT 672

Qy        655 GATGAAGATTGTGTATTGCTACTGAAAAATGGCCAGTGGAATGACGTCCCCTGCTCCACC 714
Db        673 GGGGAGCACTGTGTGACACTTCTGTCGGACGGCACATGGAATGACATCGCTTGTTCCGCC 732

Qy        715 TCCCATCTGGCCGTCTGTGAGTTCCCTATCTGA 747
Db        733 TCCTTTTTGACCGTCTGTGAATTCTCTCTCTGA 765
```

RESULT 10
US-10-764-420-2521
; Sequence 2521, Application US/10764420
; Publication No. US20050084872A1
; GENERAL INFORMATION:
; APPLICANT: Lum, Pek Yee
; APPLICANT: Tan, Yejun
; APPLICANT: Dai, Hongyue
; TITLE OF INVENTION: Methods For Determining Whether An Agent
; TITLE OF INVENTION: Possesses A Defined Biological Activity
; FILE REFERENCE: ROSA122057
; CURRENT APPLICATION NUMBER: US/10/764,420
; CURRENT FILING DATE: 2004-01-23
; PRIOR APPLICATION NUMBER: US 60/442,797
; PRIOR FILING DATE: 2003-01-24
; PRIOR APPLICATION NUMBER: US 60/474,413
; PRIOR FILING DATE: 2003-05-30
; NUMBER OF SEQ ID NOS: 3683
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2521
; LENGTH: 1069
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-764-420-2521

Query Match 50.0%; Score 373.2; DB 21; Length 1069;
Best Local Similarity 71.7%; Pred. No. 2e-111;
Matches 518; Conservative 0; Mismatches 198; Indels 6; Gaps 2;

```
Qy         26 TCCTTCTCCTGAGTATGGTGGCAGCGTCTTACTCAGAAACTGTGACCTGTGAGGATGCCC 85
Db        196 TCCTTCTGCTGTGTGTGGTGACAGTGGTTTATGCAGAGACCTTAACC---GAAGGTGTTC 252

Qy         86 AAAAGACCTGCCCTGCAGTGATTGCCTGTAGCTCTCCAGGCATCAACGGCTTCCCAGGCA 145
Db        253 AAAATTCCTGCCCT---GTGGTTACCTGCAGTTCTCCAGGCCTGAATGGCTTCCCAGGCA 309

Qy        146 AAGATGGGCGTGATGGCACCAAGGGAGAAAAGGGGGAACCAGGCCAAGGGCTCAGAGGCT 205
```

```
Db        310 AAGATGGACGTGACGGTGCCAAGGGAGAAAAGGGAGAACCAGGTCAAGGGCTCAGAGGCT 369

Qy        206 TACAGGGCCCCCCTGGAAAGTTGGGGCCTCCAGGAAATCCAGGGCCTTCTGGGTCACCAG 265

Db        370 TGCAAGGCCCTCCTGGAAAAGTAGGACCTACAGGACCCCCAGGGAATCCGGGGTTAAAAG 429

Qy        266 GACCAAAGGGCCAAAAAGGAGACCCTGGAAAAAGTCCGGATGGTGATAGTAGCCTGGCTG 325

Db        430 GAGCAGTGGGACCGAAAGGAGACCGTGGGGACAGAGCAGAATTTGATACTAGCGAAATTG 489

Qy        326 CCTCAGAAAGAAAAGCTCTGCAAACAGAAATGGCACGTATCAAAAAGTGGCTGACCTTCT 385

Db        490 ATTCAGAAATTGCAGCCCTACGATCAGAGCTGAGAGCCCTGAGAAACTGGGTGCTCTTCT 549

Qy        386 CTCTGGGCAAACAAGTTGGGAACAAGTTCTTCCTGACCAATGGTGAAATAATGACCTTTG 445

Db        550 CTCTGAGTGAAAAAGTTGGAAAGAAGTATTTTGTGAGCAGTGTTAAAAAGATGAGCCTTG 609

Qy        446 AAAAAGTGAAGGCCTTGTGTGTCAAGTTCCAGGCCTCTGTGGCCACCCCCAGGAATGCTG 505

Db        610 ACAGAGTGAAGGCCCTGTGCTCCGAATTCCAGGGCTCTGTGGCCACTCCCAGGAATGCTG 669

Qy        506 CAGAGAATGGAGCCATTCAGAATCTCATCAAGGAGGAAGCCTTCCTGGGCATCACTGATG 565

Db        670 AGGAAAACTCGGCCATCCAGAAAGTGGCCAAAGATATTGCCTACTTGGGCATCACAGATG 729

Qy        566 AGAAGACAGAAGGGCAGTTTGTGGATCTGACAGGAAATAGACTGACCTACACAAACTGGA 625

Db        730 TGAGGGTTGAAGGCAGTTTTGAGGATCTGACAGGAAACAGAGTGCGCTATACTAATTGGA 789

Qy        626 ACGAGGGTGAACCCAACAATGCTGGTTCTGATGAAGATTGTGTATTGCTACTGAAAAATG 685

Db        790 ATGATGGGGAGCCCAACAACACGGGCGATGGGGAAGACTGTGTGGTGATCTTGGGAAATG 849

Qy        686 GCCAGTGGAATGACGTCCCCTGCTCCACCTCCCATCTGGCCGTCTGTGAGTTCCCTATCT 745

Db        850 GCAAGTGGAACGATGTCCCCTGCTCTGACTCTTTTTTGGCAATCTGTGAATTCTCTGACT 909

Qy        746 GA 747

Db        910 GA 911


RESULT 11
US-09-917-800A-1710
; Sequence 1710, Application US/09917800A
; Patent No. US20020119462A1
; GENERAL INFORMATION:
;  APPLICANT: Mendrick, Donna
;  APPLICANT:  Porter, Mark
;  APPLICANT:  Johnson, Kory
;  APPLICANT:  Castle, Arthur
;  APPLICANT:  Elashoff, Michael
;  APPLICANT:  Gene Logic, Inc.
;  TITLE OF INVENTION: Molecular Toxicology Modeling
;  FILE REFERENCE: 44921-5038-US
;  CURRENT APPLICATION NUMBER: US/09/917,800A
;  CURRENT FILING DATE:  2001-07-31
;  PRIOR APPLICATION NUMBER: US 60/222,040
;  PRIOR FILING DATE: 2000-07-31
;  PRIOR APPLICATION NUMBER: US 60/222,880
;  PRIOR FILING DATE: 2000-11-02
;  PRIOR APPLICATION NUMBER: US 60/290,029
;  PRIOR FILING DATE: 2001-05-11
;  PRIOR APPLICATION NUMBER: US 60/290,645
;  PRIOR FILING DATE: 2001-05-15
;  PRIOR APPLICATION NUMBER: US 60/292,336
;  PRIOR FILING DATE: 2001-05-22
;  PRIOR APPLICATION NUMBER: US 60/295,798
;  PRIOR FILING DATE: 2001-06-06
;  PRIOR APPLICATION NUMBER: US 60/297,457
;  PRIOR FILING DATE: 2001-06-13
;  PRIOR APPLICATION NUMBER: US 60/298,884
;  PRIOR FILING DATE: 2001-06-19
;  PRIOR APPLICATION NUMBER: US 60/303,459
;  PRIOR FILING DATE: 2001-07-09
;  NUMBER OF SEQ ID NOS: 1740
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1710
;   LENGTH: 1037
;   TYPE: DNA
;   ORGANISM: Rattus norvegicus
;   FEATURE:
;   OTHER INFORMATION: Genbank Accession No. US20020119462A1 NM_022704
US-09-917-800A-1710

  Query Match             48.8%;  Score 364.6;  DB 9;  Length 1037;
  Best Local Similarity   70.7%;  Pred. No. 1.3e-108;
  Matches  483;  Conservative    0;  Mismatches  200;  Indels    0;  Gaps    0;

Qy         65 CTGTGACCTGTGAGGATGCCCAAAAGACCTGCCCTGCAGTGATTGCCTGTAGCTCTCCAG 124

Db        233 CCGAGACCTTAACCGAAGGGGCTCAAAGTAGCTGCCCTGTGATTGCCTGCAGTTCTCCGG 292

Qy        125 GCATCAACGGCTTCCCAGGCAAAGATGGGCGTGATGGCACCAAGGGAGAAAAGGGGGAAC 184

Db        293 CCTGGAACGGCTTCCCAGGCAAAGATGGACACGACGGTGCCAAGGGAGAAAAGGGAGAAC 352

Qy        185 CAGGCCAAGGGCTCAGAGGCTTACAGGGCCCCCCTGGAAAGTTGGGGCCTCCAGGAAATC 244

Db        353 CGGGTCAAGGCCTCAGAGGCTTGCAGGGCCCTCCTGGAAAAGTAGGACCTGCAGGGCCCC 412

Qy        245 CAGGGCCTTCTGGGTCACCAGGACCAAAGGGCCAAAAAGGAGACCCTGGAAAAAGTCCGG 304

Db        413 CAGGGAATCCTGGGTCAAAAGGAGCAACGGGACCAAAAGGAGACCGTGGAGAGAGTGTAG 472

Qy        305 ATGGTGATAGTAGCCTGGCTGCCTCAGAAAGAAAAGCTCTGCAAACAGAAATGGCACGTA 364

Db        473 AATTTGATACTACCAACATTGATTTAGAAATTGCAGCCCTGCGATCGGAGCTGAGAGCTA 532

Qy        365 TCAAAAAGTGGCTGACCTTCTCTCTGGGCAAACAAGTTGGGAACAAGTTCTTCCTGACCA 424

Db        533 TGAGAAAGTGGGTGCTCCTTTCTATGAGTGAAAATGTTGGAAAGAAGTACTTCATGAGCA 592

Qy        425 ATGGTGAAATAATGACCTTTGAAAAAGTGAAGGCCTTGTGTGTCAAGTTCCAGGCCTCTG 484

Db        593 GTGTTAGAAGGATGCCCCTTAACAGAGCGAAGGCTCTGTGCTCCGAACTCCAGGGCACTG 652

Qy        485 TGGCCACCCCCAGGAATGCTGCAGAGAATGGAGCCATTCAGAATCTCATCAAGGAGGAAG 544

Db        653 TGGCCACTCCCAGGAATGCTGAGGAAAATAGGGCCATCCAGAATGTGGCCAAAGATGTTG 712

Qy        545 CCTTCCTGGGCATCACTGATGAGAAGACAGAAGGGCAGTTTGTGGATCTGACAGGAAATA 604

Db        713 CCTTCTTGGGCATAACGGACCAGAGGACTGAAAACGTTTTTGAGGACCTGACAGGAAACA 772

Qy        605 GACTGACCTACACAAACTGGAACGAGGGTGAACCCAACAATGCTGGTTCTGATGAAGATT 664

Db        773 GAGTGCGCTACACTAACTGGAATGAGGGTGAGCCCAACAATGTGGGCTCTGGGGAAAACT 832

Qy        665 GTGTATTGCTACTGAAAAATGGCCAGTGGAATGACGTCCCCTGCTCCACCTCCCATCTGG 724

Db        833 GTGTGGTGCTCTTGACAAATGGGAAGTGGAATGACGTTCCTTGCTCTGATTCCTTTTTGG 892

Qy        725 CCGTCTGTGAGTTCCCTATCTGA 747

Db        893 TAGTTTGTGAATTCTCTGACTGA 915


RESULT 12
US-10-388-934-107
; Sequence 107, Application US/10388934
; Publication No. US20040005547A1
; GENERAL INFORMATION:
;  APPLICANT: Boess, Franziska
;  APPLICANT:  Suter-Dick, Laura
```

```
;  APPLICANT:  Wolf, Detlef
;  TITLE OF INVENTION: BIOMARKERS AND EXPRESSION PROFILES FOR TOXICOLOGY
;  FILE REFERENCE: 21199
;  CURRENT APPLICATION NUMBER: US/10/388,934
;  CURRENT FILING DATE:  2003-03-14
;  PRIOR APPLICATION NUMBER: 02005336.9
;  PRIOR FILING DATE: 2002-03-14
;  PRIOR APPLICATION NUMBER: 02015657.6
;  PRIOR FILING DATE: 2002-07-17
;  NUMBER OF SEQ ID NOS: 862
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 107
;   LENGTH: 1068
;   TYPE: DNA
;   ORGANISM: Rattus sp.
US-10-388-934-107

  Query Match            38.5%;  Score 287.6;  DB 17;  Length 1068;
  Best Local Similarity  68.1%;  Pred. No. 2.6e-83;
  Matches  417;  Conservative    0;  Mismatches  189;  Indels    6;  Gaps    1;

Qy        142 GGCAAAGATGGGCGTGATGGCACCAAGGGAGAAAAGGGGGAACCAGGCCAAGGGCTCAGA 201
              |||| ||| ||| | |||||  |||| || || ||||| |||||||| ||||||||||
Db         64 GGCAGAGACGGGAGAGATGGGCCCAAAGGGGAGAAGGGAGAACCAGGTCAAGGGCTCAGG 123

Qy        202 GGCTTACAGGGCCCCCCTGGAAAGTTGGGGCCTCCAGGAAATCCAGGGCCTTCTGGGTCA 261
              ||||| |||||||| || || ||  |||||||||||||||| |   |||  |  ||||
Db        124 GGCTTGCAGGGCCCTCCAGGGAAACTGGGGCCTCCAGGAAGTGTAGGAGCCCCTGGAAGT 183

Qy        262 CCAGGACCAAAGGGCCAAAAAGGAGACCCTGGAAAAAGTCCGGATGGTGATAGTAGCCTG 321
              | |||||||||| |||||||||| || | |||| | ||    |   |||    |  |||
Db        184 CAAGGACCAAAAGGCCAAAAAGGGGATCGTGGAGACAGCAGAGCCATTGAGGTGAAGCTG 243

Qy        322 GC------TGCCTCAGAAAGAAAAGCTCTGCAAACAGAAATGGCACGTATCAAAAAGTGG 375
              ||      |   |||| | |||  | ||| | || || |||  |  | ||| |||| |
Db        244 GCAAATATGGAGGCAGAGATAAACACCCTGAAGTCAAAACTGGAGCTAACCAACAAGTTG 303

Qy        376 CTGACCTTCTCTCTGGGCAAACAAGTTGGGAACAAGTTCTTCCTGACCAATGGTGAAATA 435
              |   ||||||| |||| ||| |   |||||| |||||||| |||||||   |||||
Db        304 CATGCCTTCTCCATGGGTAAAAAGTCTGGGAAGAAGTTCTTTGTGACCAACCATGAAAGG 363

Qy        436 ATGACCTTTGAAAAAGTGAAGGCCTTGTGTGTCAAGTTCCAGGCCTCTGTGGCCACCCCC 495
              ||| |||||   ||||| |||||| |||     || |||  | | |||||| | ||||
Db        364 ATGCCCTTTTCCAAAGTCAAGGCCCTGTGCTCAGAGCTCCGAGGCACTGTGGCTATCCCC 423

Qy        496 AGGAATGCTGCAGAGAATGGAGCCATTCAGAATCTCATCAAGGAGGAAGCCTTCCTGGGC 555
              |||||||||| |||||     ||||| ||  |  |     ||       |||||||| |||
Db        424 AGGAATGCTGAGGAGAACAAGGCCATCCAAGAAGTGGCTAAAACCTCTGCCTTCCTAGGC 483

Qy        556 ATCACTGATGAGAAGACAGAAGGGCAGTTTGTGGATCTGACAGGAAATAGACTGACCTAC 615
              ||||| || |||  ||| ||||| || ||  || || |||||||     || || ||||||
Db        484 ATCACGGACGAGGTGACTGAAGGCCAATTCATGTATGTGACAGGGGGGAGGCTCACCTAC 543

Qy        616 ACAAACTGGAACGAGGGTGAACCCAACAATGCTGGTTCTGATGAAGATTGTGTATTGCTA 675
              |  |||||||  ||| ||| |||||  |   ||| ||||  ||||| |||||      ||
Db        544 AGCAACTGGAAAAAGGATGAGCCCAATGACCATGGCTCTGGGGAAGACTGTGTCACTATA 603

Qy        676 CTGAAAAATGGCCAGTGGAATGACGTCCCCTGCTCCACCTCCCATCTGGCCGTCTGTGAG 735
              |  | || || | |||||||||| || |||||     | |||||   ||| ||||| |||
Db        604 GTAGACAACGGTCTGTGGAATGACATCTCCTGCCAAGCTTCCCACACGGCTGTCTGCGAG 663

Qy        736 TTCCCTATCTGA 747
              |||||   ||||
Db        664 TTCCCAGCCTGA 675


RESULT 13
US-09-960-352-11785
; Sequence 11785, Application US/09960352
; Patent No. US20020137139A1
; GENERAL INFORMATION:
;  APPLICANT: Warren, Wesley C.
;  APPLICANT:  Tao, Nengbing
;  APPLICANT:  Byatt, John C.
;  APPLICANT:  Mathialagan, Nagappan
;  TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
;  TITLE OF INVENTION:  MUSCLE AND FAT DEPOSITION
;  FILE REFERENCE: 16511.006/37-21(10298)C
;  CURRENT APPLICATION NUMBER: US/09/960,352
;  CURRENT FILING DATE:  2001-09-24
;  NUMBER OF SEQ ID NOS: 15112
; SEQ ID NO 11785
;   LENGTH: 419
;   TYPE: DNA
;   ORGANISM: Bos taurus
;   OTHER INFORMATION: Clone ID: 50-LIB34-061-Q1-E1-E6
US-09-960-352-11785

  Query Match            29.7%;  Score 222;  DB 9;  Length 419;
  Best Local Similarity  78.3%;  Pred. No. 6e-62;
  Matches  307;  Conservative    0;  Mismatches   75;  Indels   10;  Gaps    3;

Qy          1 ATGTCCCTGTTTCCATCACTCCCTCTCCTTCTCCTGAGTATGGTGGCAGCGTCTT----- 55
              ||||| |||||| ||||||| ||| | |||||||||| |  |||| |||| ||||
Db         31 ATGTCGCTGTTTACATCACTTCCTTTTCTTCTCCTGACTGCGGTGACAGCATCTTGTGCA 90

Qy         56 -ACTCAGAAACTGTGACCTGTGAGGATGCCCAAAAGACCTGCCCTGCAGTGATTGCCTGT 114
               || ||||||| | || ||||||| |   ||  |||||||||   | ||||||||||||
Db         91 GACACAGAAACAGAGAACTGTGAGAACATCCGGAAGACCTGCC---CCGTGATTGCCTGT 147

Qy        115 AGCTCTCCAGGCATCAACGGCTTCCCAGGCAAAGATGGGCGTGATGGCACCAAGGGAGAA 174
              |  |||| |||||||| ||| ||||||||||||||||||||||||  ||||||||||||
Db        148 GGTCCTCCGGGCATCAATGGCATCCCAGGCAAAGATGGGCGTGATGGTGCCAAGGGAGAA 207

Qy        175 AAGGGGGAACCAGGCCAAGGGCTCAGAGGCTTACAGGGCCCCCCTGGAAAGTTGGGGCCT 234
              ||||| |||||||| ||||| |||||||||| |||||||||||||||||| ||||||||
Db        208 AAGGGAGAACCAGGTCAAGGACTCAGAGGCTCGCAGGGCCCCCCTGGAAAGATGGGGCCT 267

Qy        235 CCAGGAAATCCAGGGCCTTCTGGGTCACCAGGACCAAAGGGCCAAAAAGGAGACCCTGGA 294
              | |||||  ||||||    |||||  |||||||||||  ||||||||||||||||||||
Db        268 CAAGGAACGCCAGGGATCCCTGGGATACCAGGACCAATAGGCCAAAAAGGAGACCCTGGA 327

Qy        295 AAAAGTCCGGATGGTGATAGTAGCCTGGCTGCCTCAGAAA-GAAAAGCTCTGCAAACAGA 353
              |||  |  || ||   ||| | |||||||| ||| | |||  ||  |  ||| ||| | ||
Db        328 GAAAATATGGGTGACTATATTCGCCTGGCTACCTTAAAAAGGAGCAATTCTACAATCTGA 387

Qy        354 AATGGCACGTATCAAAAAGTGGCTGACCTTCT 385
              | ||    |  |||||||| ||||| | |||||
Db        388 ATTGAACCAGATCAAAAACTGGCTAATCTTCT 419


RESULT 14
US-10-450-472-58
; Sequence 58, Application US/10450472
; Publication No. US20040132094A1
; GENERAL INFORMATION:
;  APPLICANT: Borean Pharma A/S
;  TITLE OF INVENTION: Combinatorial libraries of proteins having the scaffold structur
;  TITLE OF INVENTION:  of C-type lectin-like domains
;  FILE REFERENCE: BOR00003/WO
;  CURRENT APPLICATION NUMBER: US/10/450,472
;  CURRENT FILING DATE:  2003-12-08
;  NUMBER OF SEQ ID NOS: 91
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 58
;   LENGTH: 405
;   TYPE: DNA
;   ORGANISM: Rattus rattus
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (8)..(400)
;   OTHER INFORMATION: Rat PrMBP insert
US-10-450-472-58

  Query Match            24.9%;  Score 186.2;  DB 19;  Length 405;
  Best Local Similarity  68.5%;  Pred. No. 3.4e-50;
```

```
  Matches  257;  Conservative    0;  Mismatches  118;  Indels    0;  Gaps    0;

Qy        366 CAAAAAGTGGCTGACCTTCTCTCTGGGCAAACAAGTTGGGAACAAGTTCTTCCTGACCAA 425
              ||| |||| ||   |||||||  |||| ||| |   |||||| ||||||||  |||||||
Db         19 CAACAAGTTGCATGCCTTCTCCATGGGTAAAAAGTCTGGGAAGAAGTTCTTTGTGACCAA 78

Qy        426 TGGTGAAATAATGACCTTTGAAAAAGTGAAGGCCTTGTGTGTCAAGTTCCAGGCCTCTGT 485
              |||||  ||| |||||   ||||| |||||| ||||    || |||  | | ||||
Db         79 CCATGAAAGGATGCCCTTTTCCAAAGTCAAGGCCCTGTGCTCAGAGCTCCGAGGCACTGT 138

Qy        486 GGCCACCCCCAGGAATGCTGCAGAGAATGGAGCCATTCAGAATCTCATCAAGGAGGAAGC 545
              ||| | ||||| ||||||||  |||||    ||||| ||  |  |    ||        ||
Db        139 GGCTATCCCCAAGAATGCTGAGGAGAACAAGGCCATCCAAGAAGTGGCTAAAACCTCTGC 198

Qy        546 CTTCCTGGGCATCACTGATGAGAAGACAGAAGGGCAGTTTGTGGATCTGACAGGAAATAG 605
              |||||| |||||||| || |||  ||| ||||| || ||  || || |||||||    ||
Db        199 CTTCCTAGGCATCACGGACGAGGTGACTGAAGGCCAATTCATGTATGTGACAGGGGGGAG 258

Qy        606 ACTGACCTACACAAACTGGAACGAGGGTGAACCCAACAATGCTGGTTCTGATGAAGATTG 665
              || |||||||  ||||||||  ||| ||| |||||  |   ||| ||||  ||||| ||
Db        259 GCTCACCTACAGCAACTGGAAAAAGGATGAGCCCAATGACCATGGCTCTGGGGAAGACTG 318

Qy        666 TGTATTGCTACTGAAAAATGGCCAGTGGAATGACGTCCCCTGCTCCACCTCCCATCTGGC 725
              |||     || |  | || || | |||||||||| || |||||    | |||||   |||
Db        319 TGTCACTATAGTAGACAACGGTCTGTGGAATGACATCTCCTGCCAAGCTTCCCACACGGC 378

Qy        726 CGTCTGTGAGTTCCC 740
              ||||| ||||||||
Db        379 TGTCTGCGAGTTCCC 393


RESULT 15
US-10-070-415A-45
; Sequence 45, Application US/10070415A
; Publication No. US20040043379A1
; GENERAL INFORMATION:
;  APPLICANT: HASHIMOTO, Koji
;  APPLICANT:  ASHIMOTO, Michie
;  APPLICANT:  MISHIRO, Shunji
;  APPLICANT:  OOTA, Yasuhiko
;  TITLE OF INVENTION: DETECTION OF NUCLEIC ACID ASSOCIATED WITH DISEASE
;  FILE REFERENCE: 220633US2SRDPCT
;  CURRENT APPLICATION NUMBER: US/10/070,415A
;  CURRENT FILING DATE:  2003-07-23
;  PRIOR APPLICATION NUMBER: PCT/JP02/02030
;  PRIOR FILING DATE: 2002-03-05
;  PRIOR APPLICATION NUMBER: JP 2001-090053
;  PRIOR FILING DATE: 2001-03-27
;  PRIOR APPLICATION NUMBER: JP 2001-284112
;  PRIOR FILING DATE: 2001-09-18
;  NUMBER OF SEQ ID NOS: 72
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 45
;   LENGTH: 1802
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (96)..(96)
;   OTHER INFORMATION: n is a nucleotide selected from a, g, c, or t
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (649)..(649)
;   OTHER INFORMATION: n is a nucleotide selected from a, g, c, or t
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (868)..(868)
;   OTHER INFORMATION: n is a nucleotide selected from a, g, c, or t
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (884)..(884)
;   OTHER INFORMATION: n is a nucleotide selected from a, g, c, or t
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (425)..(425)
;   OTHER INFORMATION: n is a nucleotide selected from a, g, c, or t
US-10-070-415A-45

  Query Match           24.9%;  Score 186;  DB 18;  Length 1802;
  Best Local Similarity  98.9%;  Pred. No. 7.8e-50;
  Matches  186;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 ATGTCCCTGTTTCCATCACTCCCTCTCCTTCTCCTGAGTATGGTGGCAGCGTCTTACTCA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        715 ATGTCCCTGTTTCCATCACTCCCTCTCCTTCTCCTGAGTATGGTGGCAGCGTCTTACTCA 774

Qy         61 GAAACTGTGACCTGTGAGGATGCCCAAAAGACCTGCCCTGCAGTGATTGCCTGTAGCTCT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        775 GAAACTGTGACCTGTGAGGATGCCCAAAAGACCTGCCCTGCAGTGATTGCCTGTAGCTCT 834

Qy        121 CCAGGCATCAACGGCTTCCCAGGCAAAGATGGGCGTGATGGCACCAAGGGAGAAAAGGGG 180
              |||||||||||||||||||||||||||||||| |||||||||||||| ||||||||||
Db        835 CCAGGCATCAACGGCTTCCCAGGCAAAGATGGGNGTGATGGCACCAAGGNAGAAAAGGGG 894

Qy        181 GAACCAGG 188
              ||||||||
Db        895 GAACCAGG 902


Search completed: June 20, 2005, 19:30:53
Job time : 1646 secs
```

THIS PAGE BLANK (USPTO)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 20, 2005, 03:04:56 ; Search time 3223 Seconds
(without alignments)
8822.218 Million cell updates/sec

Title: US-10-054-536-2
Perfect score: 747
Sequence: 1 atgtccctgtttccatcact.....tctgtgagttccctatctga 747

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*
1: gb_est1:*
2: gb_est2:*
3: gb_htc:*
4: gb_est3:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_gss1:*
9: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.		Score	% Query Match	Length	DB	ID	Description
1		678	90.8	747	9	AY413286	AY413286 Homo sapi
2		671.6	89.9	747	9	AY413287	AY413287 Pan trogl
3		668.6	89.5	1000	7	CO579105	CO579105 ILLUMIGEN
4		644.6	86.3	968	7	CO579085	CO579085 ILLUMIGEN
5		394.4	52.8	807	7	CO738739	CO738739 SlLE04c21
6		352.2	47.1	735	9	AY413288	AY413288 Mus muscu
7		338.6	45.3	977	7	CO583176	CO583176 ILLUMIGEN
8		335	44.8	828	2	BF537636	BF537636 602054516
9	c	324.8	43.5	722	7	CK778513	CK778513 965675 MA
10		303	40.6	367	1	AV660023	AV660023 AV660023
11		302.2	40.5	657	1	AI255533	AI255533 ui55f12.y
12		301.4	40.3	1162	3	AY325174	AY325174 Rattus no
13		301.4	40.3	1162	3	AY325178	AY325178 Rattus no
14	c	292.4	39.1	869	1	AI195233	AI195233 ui62c03.x
15		291	39.0	367	1	AV660367	AV660367 AV660367
16	c	290.4	38.9	789	1	AI174038	AI174038 ud67a02.x
17		286	38.3	1565	3	AK034788	AK034788 Mus muscu
18		283.6	38.0	772	7	CO812153	CO812153 AGENCOURT
19		276	36.9	896	7	CO809875	CO809875 AGENCOURT
20		268.4	35.9	557	2	BE682267	BE682267 180230 MA
21		268	35.9	788	4	BI147944	BI147944 602912658
22	c	267.6	35.8	784	1	AI173576	AI173576 ud68d03.x
23	c	258.4	34.6	777	1	AI194713	AI194713 ui55f12.x
24		257	34.4	956	6	CA479090	CA479090 AGENCOURT
25		256.6	34.4	664	1	AI876217	AI876217 uj59d03.y
26	c	256	34.3	592	1	AI786738	AI786738 uj56d08.x
27		255.6	34.2	832	6	CB948709	CB948709 AGENCOURT
28		250.2	33.5	957	6	CA478654	CA478654 AGENCOURT
29		248.4	33.3	627	7	CF179019	CF179019 813103 MA
30		246.2	33.0	738	4	BI144334	BI144334 602908384
31		245.8	32.9	540	5	BX526094	BX526094 BX526094
32		243.4	32.6	753	4	BI145807	BI145807 602909275
33		242.6	32.5	799	1	AI097858	AI097858 ue40g03.y
34	c	242.2	32.4	653	7	CO675645	CO675645 DG42-172i
35		242	32.4	566	7	CO775884	CO775884 ILLUMIGEN
36		240.4	32.2	949	6	CA479163	CA479163 AGENCOURT
37	c	239.8	32.1	677	1	AI118440	AI118440 ue40g03.x
38		239.4	32.0	476	2	BF652528	BF652528 276116 MA
39		239	32.0	653	6	CB419261	CB419261 592111 MA
40	c	236.4	31.6	605	7	CO676106	CO676106 DG42-184f
41		236.4	31.6	758	1	AV649316	AV649316 AV649316
42	c	235.8	31.6	619	7	CO674631	CO674631 DG42-144g
43		234.8	31.4	393	1	AV649531	AV649531 AV649531
44	c	234	31.3	611	7	CO674696	CO674696 DG42-146b
45		231.6	31.0	760	6	CB947613	CB947613 AGENCOURT

ALIGNMENTS

RESULT 1
AY413286
LOCUS AY413286 747 bp DNA linear GSS 17-DEC-2003
DEFINITION Homo sapiens MBL2 gene, VIRTUAL TRANSCRIPT, partial sequence, genomic survey sequence.
ACCESSION AY413286
VERSION AY413286.1 GI:39769248
KEYWORDS GSS.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 747)
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.
TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous gene trios
JOURNAL Science 302 (5652), 1960-1963 (2003)
PUBMED 14671302
REFERENCE 2 (bases 1 to 747)
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.
TITLE Direct Submission
JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA
COMMENT This sequence was made by sequencing genomic exons and ordering them based on alignment.
FEATURES Location/Qualifiers
source 1. .747
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
gene <1. .>747
/gene="MBL2"
/locus_tag="HCM4840"
ORIGIN

Query Match 90.8%; Score 678; DB 9; Length 747;
Best Local Similarity 90.8%; Pred. No. 1.4e-182;
Matches 678; Conservative 0; Mismatches 69; Indels 0; Gaps 0;

Qy 1 ATGTCCCTGTTTCCATCACTCCCTCTCCTTCTCCTGAGTATGGTGGCAGCGTCTTACTCA 60
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

```
Db          1 ATGTCCCTGTTTCCATCACTCCCTCTCCTTCTCCTGAGTATGGTGGCAGCGTCTTACTCA 60

Qy         61 GAAACTGTGACCTGTGAGGATGCCCAAAAGACCTGCCCTGCAGTGATTGCCTGTAGCTCT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GAAACTGTGACCTGTGAGGATGCCCAAAAGACCTGCCCTGCAGTGATTGCCTGTAGCTCT 120

Qy        121 CCAGGCATCAACGGCTTCCCAGGCAAAGATGGGCGTGATGGCACCAAGGGAGAAAAGGGG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CCAGGCATCAACGGCTTCCCAGGCAAAGATGGGCGTGATGGCACCAAGGGAGAAAAGGGG 180

Qy        181 GAACCAGGCCAAGGGCTCAGAGGCTTACAGGGCCCCCCTGGAAAGTTGGGGCCTCCAGGA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GAACCAGGCCAAGGGCTCAGAGGCTTACAGGGCCCCCCTGGAAAGTTGGGGCCTCCAGGA 240

Qy        241 AATCCAGGGCCTTCTGGGTCACCAGGACCAAAGGGCCAAAAAGGAGACCCTGGAAAAAGT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 AATCCAGGGCCTTCTGGGTCACCAGGACCAAAGGGCCAAAAAGGAGACCCTGGAAAAAGT 300

Qy        301 CCGGATGGTGATAGTAGCCTGGCTGCCTCAGAAAGAAAAGCTCTGCAAACAGAAATGGCA 360
              ||||
Db        301 CCGGNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 360

Qy        361 CGTATCAAAAAGTGGCTGACCTTCTCTCTGGGCAAACAAGTTGGGAACAAGTTCTTCCTG 420
                          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 NNNNNNNNNNNNNGGCTGACCTTCTCTCTGGGCAAACAAGTTGGGAACAAGTTCTTCCTG 420

Qy        421 ACCAATGGTGAAATAATGACCTTTGAAAAAGTGAAGGCCTTGTGTGTCAAGTTCCAGGCC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 ACCAATGGTGAAATAATGACCTTTGAAAAAGTGAAGGCCTTGTGTGTCAAGTTCCAGGCC 480

Qy        481 TCTGTGGCCACCCCCAGGAATGCTGCAGAGAATGGAGCCATTCAGAATCTCATCAAGGAG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 TCTGTGGCCACCCCCAGGAATGCTGCAGAGAATGGAGCCATTCAGAATCTCATCAAGGAG 540

Qy        541 GAAGCCTTCCTGGGCATCACTGATGAGAAGACAGAAGGGCAGTTTGTGGATCTGACAGGA 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GAAGCCTTCCTGGGCATCACTGATGAGAAGACAGAAGGGCAGTTTGTGGATCTGACAGGA 600

Qy        601 AATAGACTGACCTACACAAACTGGAACGAGGGTGAACCCAACAATGCTGGTTCTGATGAA 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 AATAGACTGACCTACACAAACTGGAACGAGGGTGAACCCAACAATGCTGGTTCTGATGAA 660

Qy        661 GATTGTGTATTGCTACTGAAAAATGGCCAGTGGAATGACGTCCCCTGCTCCACCTCCCAT 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 GATTGTGTATTGCTACTGAAAAATGGCCAGTGGAATGACGTCCCCTGCTCCACCTCCCAT 720

Qy        721 CTGGCCGTCTGTGAGTTCCCTATCTGA 747
              ||||||||||||||||||||||||||
Db        721 CTGGCCGTCTGTGAGTTCCCTATCTGA 747
```

```
RESULT 2
AY413287
LOCUS       AY413287                747 bp    DNA     linear   GSS 17-DEC-2003
DEFINITION  Pan troglodytes MBL2 gene, VIRTUAL TRANSCRIPT, partial sequence,
            genomic survey sequence.
ACCESSION   AY413287
VERSION     AY413287.1  GI:39769249
KEYWORDS    GSS.
SOURCE      Pan troglodytes (chimpanzee)
  ORGANISM  Pan troglodytes
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
REFERENCE   1  (bases 1 to 747)
  AUTHORS   Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
            Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
            Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
            Adams,M.D. and Cargill,M.
  TITLE     Inferring nonneutral evolution from human-chimp-mouse orthologous
            gene trios
  JOURNAL   Science 302 (5652), 1960-1963 (2003)
   PUBMED   14671302
REFERENCE   2  (bases 1 to 747)
  AUTHORS   Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
            Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
            Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
            Adams,M.D. and Cargill,M.
  TITLE     Direct Submission
  JOURNAL   Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
            Rockville, MD 20850, USA
COMMENT     This sequence was made by sequencing genomic exons and ordering
            them based on alignment.
FEATURES             Location/Qualifiers
     source          1. .747
                     /organism="Pan troglodytes"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9598"
     gene            <1. .>747
                     /gene="MBL2"
                     /locus_tag="HCM4840"
ORIGIN
```

Query Match 89.9%; Score 671.6; DB 9; Length 747;
Best Local Similarity 90.2%; Pred. No. 9.6e-181;
Matches 674; Conservative 0; Mismatches 73; Indels 0; Gaps 0;

```
Qy          1 ATGTCCCTGTTTCCATCACTCCCTCTCCTTCTCCTGAGTATGGTGGCAGCGTCTTACTCA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGTCCCTGTTTCCATCACTCCCTCTCCTTCTCCTGAGTATGGTGGCAGCGTCTTACTCA 60

Qy         61 GAAACTGTGACCTGTGAGGATGCCCAAAAGACCTGCCCTGCAGTGATTGCCTGTAGCTCT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GAAACTGTGACCTGTGAGGATGCCCAAAAGACCTGCCCTGCAGTGATTGCCTGTAGCTCT 120

Qy        121 CCAGGCATCAACGGCTTCCCAGGCAAAGATGGGCGTGATGGCACCAAGGGAGAAAAGGGG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CCAGGCATCAACGGCTTCCCAGGCAAAGATGGGCGTGATGGCACCAAGGGAGAAAAGGGG 180

Qy        181 GAACCAGGCCAAGGGCTCAGAGGCTTACAGGGCCCCCCTGGAAAGTTGGGGCCTCCAGGA 240
              |||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||
Db        181 GAACCAGGCCAAGGGCTCAGAGGCTTACAGGGCCCTCCTGGAAAGTTGGGGCCTCCAGGA 240

Qy        241 AATCCAGGGCCTTCTGGGTCACCAGGACCAAAGGGCCAAAAAGGAGACCCTGGAAAAAGT 300
              |||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||
Db        241 AATCCAGGGCCTTCTGGGTCACCAGGACCAAAGGGCCAGAAAGGAGACCCTGGAAAAAGT 300

Qy        301 CCGGATGGTGATAGTAGCCTGGCTGCCTCAGAAAGAAAAGCTCTGCAAACAGAAATGGCA 360
              ||||
Db        301 CCGGNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 360

Qy        361 CGTATCAAAAAGTGGCTGACCTTCTCTCTGGGCAAACAAGTTGGGAACAAGTTCTTCCTG 420
                          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 NNNNNNNNNNNNNGGCTGACCTTCTCTCTGGGCAAACAAGTTGGGAACAAGTTCTTCCTG 420

Qy        421 ACCAATGGTGAAATAATGACCTTTGAAAAAGTGAAGGCCTTGTGTGTCAAGTTCCAGGCC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 ACCAATGGTGAAATAATGACCTTTGAAAAAGTGAAGGCCTTGTGTGTCAAGTTCCAGGCC 480

Qy        481 TCTGTGGCCACCCCCAGGAATGCTGCAGAGAATGGAGCCATTCAGAATCTCATCAAGGAG 540
              |||||||||||||||||||||||||||||||| ||| ||||||||||||||||||||||
Db        481 TCTGTGGCCACCCCCAGGAATGCTGCAGAGAATGGAGCCGTTCGGAATCTCATCAAGGAG 540

Qy        541 GAAGCCTTCCTGGGCATCACTGATGAGAAGACAGAAGGGCAGTTTGTGGATCTGACAGGA 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GAAGCCTTCCTGGGCATCACTGATGAGAAGACAGAAGGGCAGTTTGTGGATCTGACAGGA 600

Qy        601 AATAGACTGACCTACACAAACTGGAACGAGGGTGAACCCAACAATGCTGGTTCTGATGAA 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 AATAGACTGACCTACACAAACTGGAACGAGGGTGAACCCAACAATGCTGGTTCTGATGAA 660

Qy        661 GATTGTGTATTGCTACTGAAAAATGGCCAGTGGAATGACGTCCCCTGCTCCACCTCCCAT 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 GATTGTGTATTGCTACTGAAAAATGGCCAGTGGAATGACGTCCCCTGCTCCACCTCCCAT 720

Qy        721 CTGGCCGTCTGTGAGTTCCCTATCTGA 747
              ||||||||||||||||||||||||||
```

```
Db        721 CTGGCCGTCTGTGAGTTCCCTATCTGA 747


RESULT 3
CO579105
LOCUS       CO579105                1000 bp    mRNA    linear   EST 20-JUL-2004
DEFINITION  ILLUMIGEN_MCQ_50626 Katze_MNLV Macaca nemestrina cDNA clone
            IBIUW:18533 5' similar to Bases 76 to 977 highly similar to human
            MBL2 (Hs.2314), mRNA sequence.
ACCESSION   CO579105
VERSION     CO579105.1  GI:50409981
KEYWORDS    EST.
SOURCE      Macaca nemestrina (pig-tailed macaque)
  ORGANISM  Macaca nemestrina
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
            Cercopithecinae; Macaca.
REFERENCE   1  (bases 1 to 1000)
  AUTHORS   Katze,M.G., Thomas,M., Korth,M., Iadonato,S.P. and Magness,C.L.
  TITLE     Large-scale Rhesus Macaque cDNA Sequencing
  JOURNAL   Unpublished (2003)
COMMENT     Contact: C. Magness
            Illumigen Biosciences Inc.
            2203 Airport Way S, Suite 450, Seattle, WA 98134, USA
            Tel: 2063780400
            Fax: 2063780408
            Email: cmagness@illumigen.com
            Sequenced on 2004.07.16. 690 Q20 bases. Library Preparation: Prof.
            Michael Katze Lab at University of Washington DNA Sequencing:
            Illumigen Biosciences Inc. For further information, see
            http://www.macaque.org
            PCR PRimers
            FORWARD: CCCTCACTAAAGGGAACAAAA
            BACKWARD: CACTATAGGGCGAATTGGGTA
            Insert Length: 1000   Std Error: 0.00
            Plate: CL000535  row: B  column: 08
            Seq primer: CCCTCACTAAAGGGAACAAAA
            POLYA=Yes.
FEATURES              Location/Qualifiers
     source           1. .1000
                      /organism="Macaca nemestrina"
                      /mol_type="mRNA"
                      /strain="Indian"
                      /db_xref="taxon:9545"
                      /clone="IBIUW:18533"
                      /sex="male"
                      /lab_host="Electromax DH10B"
                      /clone_lib="Katze_MNLV"
                      /note="Organ: liver; Vector: pDONR 222; Site_1: BsrG I;
                      Site_2: BsrG I; Created from CloneMiner cDNA Library
                      Construction kit (catalog #18249-029)"
ORIGIN

  Query Match             89.5%;  Score 668.6;  DB 7;  Length 1000;
  Best Local Similarity   93.4%;  Pred. No. 7.6e-180;
  Matches  698;  Conservative    0;  Mismatches   49;  Indels    0;  Gaps    0;

Qy          1 ATGTCCCTGTTTCCATCACTCCCTCTCCTTCTCCTGAGTATGGTGGCAGCGTCTTACTCA 60
              |||||||||||||||||||| |||||||||||||||| |||||||| | |||||||||
Db         87 ATGTCCCTGTTTCCATCACTCACTCTCCTTCTCCTGAGTGTGGTGGCAACATCTTACTCA 146

Qy         61 GAAACTGTGACCTGTGAGGATGCCCAAAAGACCTGCCCTGCAGTGATTGCCTGTAGCTCT 120
              |||||||||||||||||||| ||||||||| |||||||| |||||||||||||| |||
Db        147 GAAACTGTGACCTGTGAGGATTCCCAAAAGATCTGCCCTGCGGTGATTGCCTGTAACTCC 206

Qy        121 CCAGGCATCAACGGCTTCCCAGGCAAAGATGGGCGTGATGGCACCAAGGGAGAAAAGGGG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        207 CCAGGCATCAACGGCTTCCCAGGCAAAGATGGGCGTGATGGCACCAAGGGAGAAAAGGGG 266

Qy        181 GAACCAGGCCAAGGGCTCAGAGGCTTACAGGGCCCCCCTGGAAAGTTGGGGCCTCCAGGA 240
              |||||||||||||||||||| |||||||||| ||||||||||||||||||||||||||
Db        267 GAACCAGGCCAAGGGCTCAGAGGTTTACAGGGCCCTCCTGGAAAGTTGGGGCCTCCAGGA 326

Qy        241 AATCCAGGGCCTTCTGGGTCACCAGGACCAAAGGGCCAAAAAGGAGACCCTGGAAAAAGT 300
              ||||||||| |||||||||||||||||||||||||||||||||||||||||||| | |||
Db        327 AATCCAGGGTCTTCTGGGTCACCAGGACCAAAGGGCCAAAAAGGAGACCCTGGAGAGAGT 386

Qy        301 CCGGATGGTGATAGTAGCCTGGCTGCCTCAGAAAGAAAAGCTCTGCAAACAGAAATGGCA 360
              || ||| |||| ||||||||||||||||||||||||||||||||||||||||||||||||
Db        387 CCAGATTGTGAGAGTAGCCTGGCTGCCTCAGAAAGAAAAGCTCTGCAAACAGAAATGGCT 446

Qy        361 CGTATCAAAAAGTGGCTGACCTTCTCTCTGGGCAAACAAGTTGGGAACAAGTTCTTCCTG 420
              |||||||||||| |||||||||||||||||||||||| ||||||||||||||||||||||
Db        447 CGTATCAAAAAATGGCTGACCTTCTCTCTGGGCAGACAAGTTGGGAACAAGTTCTTCCTG 506

Qy        421 ACCAATGGTGAAATAATGACCTTTGAAAAAGTGAAGGCCTTGTGTGTCAAGTTCCAGGCC 480
              || |||||||||| |||||||||| |||||||||| |||||| | |||| ||||||
Db        507 ACTAATGGTGAAATGATGACCTTTGACAAAGTGAAGGCCCTGTGTGCCGAGTTTCAGGCC 566

Qy        481 TCTGTGGCCACCCCCAGGAATGCTGCAGAGAATGGAGCCATTCAGAATCTCATCAAGGAG 540
              |||||||||||||||||||||||||||||||||| ||||||| ||||||||||||||||
Db        567 TCTGTGGCCACCCCCAGGAATGCTGCAGAGAACAGAGCCATCCAGAATCTCATCAAGGAG 626

Qy        541 GAAGCCTTCCTGGGCATCACTGATGAGAAGACAGAAGGGCAGTTTGTGGATCTGACAGGA 600
              |||||||||||||||||||||||||||||| ||||||||| ||||||| ||||||||||||
Db        627 GAAGCCTTCCTGGGCATCACTGATGAGAACACAGAAGGGGAGTTTGTAGATCTGACAGGA 686

Qy        601 AATAGACTGACCTACACAAACTGGAACGAGGGTGAACCCAACAATGCTGGTTCTGATGAA 660
              |||| |||||||||||||||||||||||| ||||| ||||||||||||||| |||||
Db        687 AATAAACTGACCTACACAAACTGGAACGATGGTGAGCCCAACAATGCTGGTTCTAATGAA 746

Qy        661 GATTGTGTATTGCTACTGAAAAATGGCCAGTGGAATGACGTCCCCTGCTCCACCTCCCAT 720
              || ||||||||| |||||||||||||| |||||||||| |||||||||| | |||| |
Db        747 GACTGTGTATTGTTACTGAAAAATGGCAAGTGGAATGACATCCCCTGCTCCTCTTCCCTT 806

Qy        721 CTGGCCGTCTGTGAGTTCCCTATCTGA 747
              |||| | |||| || ||||||||||
Db        807 CTGGGCCTCTGCGAAGTCCCTATCTGA 833


RESULT 4
CO579085
LOCUS       CO579085                 968 bp    mRNA    linear   EST 20-JUL-2004
DEFINITION  ILLUMIGEN_MCQ_50641 Katze_MNLV Macaca nemestrina cDNA clone
            IBIUW:16614 5' similar to Bases 83 to 967 highly similar to human
            MBL2 (Hs.2314), mRNA sequence.
ACCESSION   CO579085
VERSION     CO579085.1  GI:50409957
KEYWORDS    EST.
SOURCE      Macaca nemestrina (pig-tailed macaque)
  ORGANISM  Macaca nemestrina
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
            Cercopithecinae; Macaca.
REFERENCE   1  (bases 1 to 968)
  AUTHORS   Katze,M.G., Thomas,M., Korth,M., Iadonato,S.P. and Magness,C.L.
  TITLE     Large-scale Rhesus Macaque cDNA Sequencing
  JOURNAL   Unpublished (2003)
COMMENT     Contact: C. Magness
            Illumigen Biosciences Inc.
            2203 Airport Way S, Suite 450, Seattle, WA 98134, USA
            Tel: 2063780400
            Fax: 2063780408
            Email: cmagness@illumigen.com
            Sequenced on 2004.07.16. 683 Q20 bases. Library Preparation: Prof.
            Michael Katze Lab at University of Washington DNA Sequencing:
            Illumigen Biosciences Inc. For further information, see
            http://www.macaque.org
            PCR PRimers
            FORWARD: CCCTCACTAAAGGGAACAAAA
            BACKWARD: CACTATAGGGCGAATTGGGTA
            Insert Length: 968   Std Error: 0.00
            Plate: CL000535  row: B  column: 06
            Seq primer: CCCTCACTAAAGGGAACAAAA
            POLYA=No.
FEATURES              Location/Qualifiers
```

```
     source          1. .968
                     /organism="Macaca nemestrina"
                     /mol_type="mRNA"
                     /strain="Indian"
                     /db_xref="taxon:9545"
                     /clone="IBIUW:16614"
                     /sex="male"
                     /lab_host="Electromax DH10B"
                     /clone_lib="Katze_MNLV"
                     /note="Organ: liver; Vector: pDONR 222; Site_1: BsrG I;
                     Site_2: BsrG I; Created from CloneMiner cDNA Library
                     Construction kit (catalog #18249-029)"
ORIGIN

  Query Match             86.3%;  Score 644.6;  DB 7;  Length 968;
  Best Local Similarity   93.2%;  Pred. No. 5.6e-173;
  Matches  696;  Conservative    0;  Mismatches   49;  Indels    2;  Gaps    2;

Qy          1 ATGTCCCTGTTTCCATCACTCCCTCTCCTTCTCCTGAGTATGGTGGCAGCGTCTTACTCA 60
              |||||||||||||||||||| |||||||||||||||| |||||||| | |||||||||
Db         94 ATGTCCCTGTTTCCATCACTCACTCTCCTTCTCCTGAGTGTGGTGGCAACATCTTACTCA 153

Qy         61 GAAACTGTGACCTGTGAGGATGCCCAAAAGACCTGCCCTGCAGTGATTGCCTGTAGCTCT 120
              |||||||||||||||||||| |||||||| ||||||||| |||||||||||||| |||
Db        154 GAAACTGTGACCTGTGAGGATTCCCAAAAGATCTGCCCTGCGGTGATTGCCTGTAACTCC 213

Qy        121 CCAGGCATCAACGGCTTCCCAGGCAAAGATGGGCGTGATGGCACCAAGGGAGAAAAGGGG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        214 CCAGGCATCAACGGCTTCCCAGGCAAAGATGGGCGTGATGGCACCAAGGGAGAAAAGGGG 273

Qy        181 GAACCAGGCCAAGGGCTCAGAGGCTTACAGGGCCCCCCTGGAAAGTTGGGGCCTCCAGGA 240
              |||||||||||||||||||| |||||||||| || ||||||||||||||||||||||||
Db        274 GAACCAGGCCAAGGGCTCAGAGGTTTACAGGGCCCTCCAGGAAAGTTGGGGCCTCCAGGA 333

Qy        241 AATCCAGGGCCTTCTGGGTCACCAGGACCAAAGGGCCAAAAAGGAGACCCTGGAAAAAGT 300
              ||||||||| ||||||||||||||||||||||||||||||||||||||||||| | |||
Db        334 AATCCAGGGTCTTCTGGGTCACCAGGACCAAAGGGCCAAAAAGGAGACCCTGGAGAGAGT 393

Qy        301 CCGGATGGTGATAGTAGCCTGGCTGCCTCAGAAAGAAAAGCTCTGCAAACAGAAATGGCA 360
              || ||| |||| ||||||||||||||||||||||||||||||||||||||||||||||||
Db        394 CCAGATTGTGAGAGTAGCCTGGCTGCCTCAGAAAGAAAAGCTCTGCAAACAGAAATGGCT 453

Qy        361 CGTATCAAAAAGTGGCTGACCTTCTCTCTGGGCAAACAAGTTGGGAACAAGTTCTTCCTG 420
              |||||||||| |||||||||||||||||||| |||||||||||||||||||||||||||
Db        454 CGTATCAAAAAATGGCTGACCTTCTCTCTGGGCAGACAAGTTGGGAACAAGTTCTTCCTG 513

Qy        421 ACCAATGGTGAAATAATGACCTTTGAAAAAGTGAAGGCCTTGTGTGTCAAGTTCCAGGCC 480
              || |||||||||| |||||||||| |||||||||| |||||| | |||| ||||||
Db        514 ACTAATGGTGAAATGATGACCTTTGACAAAGTGAAGGCCCTGTGTGCCGAGTTTCAGGCC 573

Qy        481 TCTGTGGCCACCCCCAGGAATGCTGCAGAGAATGGAGCCATTCAGAATCTCATCAAGGAG 540
              |||||||||||||||||||||||||||||||| |||||||| ||||||||||||||||||
Db        574 TCTGTGGCCACCCCCAGGAATGCTGCAGAGAACAGAGCCATCCAGAATCTCATCAAGGAG 633

Qy        541 GAAGCCTTCCTGGGCATCACTGATGAGAAGACAGAAGGGCAGTTTGTGGATCTGACAGGA 600
              |||||||||||||||||||||||||||||| ||||||||| ||||||| ||||||||||||
Db        634 GAAGCCTTCCTGGGCATCACTGATGAGAACACAGAAGGGGAGTTTGTAGATCTGACAGGA 693

Qy        601 AATAGACTGACCTACACAAACTGGAACGAGGGTGAACCCAACAATGCTGGTTCTGATGAA 660
              |||| |||||||||||||||||||||| ||||| ||| ||||||||||||| ||||
Db        694 AATAAACTGACCTACACAAACTGGAACGATGGTGAGCCC-ACAATGCTGGTTCTAATGAG 752

Qy        661 GATTGTGTATTGCTACTGAAAAATGGCCAGTGGAATGACGTCCCCTGCTCCACCTCCCAT 720
              | ||||||||| ||||| |||||||| |||||||||| |||||||||| | ||||||
Db        753 AACTGTGTATTGTTACTG-AAAATGGCAAGTGGAATGACATCCCCTGCTCCTCTTCCCAT 811

Qy        721 CTGGCCGTCTGTGAGTTCCCTATCTGA 747
              |||||| |||| || ||||||||||||
Db        812 CTGGCCCTCTGCGATTTCCCTATCTGA 838


RESULT 5
CO738739
```

```
LOCUS       CO738739                807 bp    mRNA    linear   EST 29-JUL-2004
DEFINITION  S1LE04c21f10f1 squirrel embryo library 1 Spermophilus lateralis
            cDNA clone 21f10 5', mRNA sequence.
ACCESSION   CO738739
VERSION     CO738739.1  GI:50826009
KEYWORDS    EST.
SOURCE      Spermophilus lateralis (golden-mantled ground squirrel)
  ORGANISM  Spermophilus lateralis
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Sciuridae; Sciurinae;
            Spermophilus.
REFERENCE   1  (bases 1 to 807)
  AUTHORS   Williams,D.R., Gracey,A.Y., Martin,S.L., Hughes,M.A., Li,W.,
            Rogers,J. and Cossins,A.R.
  TITLE     Microarray analysis of transcriptional changes during hibernation
            in the golden mantled ground squirrel, Spermophilus lateralis
  JOURNAL   Unpublished (2004)
COMMENT     Contact: Andrew R. Cossins
            Laboratory for Environmental Gene Regulation
            University of Liverpool
            School of Biological Sciences, The Biosciences Building, Crown
            Street, Liverpool, United Kingdom, L69 7ZB
            Tel: +44(0)151-795-4510
            Fax: +44(0)151-795-4431
            Email: cossins@liv.ac.uk
            Vector has been trimmed from this EST.
            Plate: 21  row: f  column: 10
            Seq primer: pflc T7 (5'-AATACGACTCACTATAGGG-3')
            High quality sequence stop: 807.
FEATURES             Location/Qualifiers
     source          1. .807
                     /organism="Spermophilus lateralis"
                     /mol_type="mRNA"
                     /db_xref="taxon:76772"
                     /clone="21f10"
                     /sex="male and female"
                     /tissue_type="embryo"
                     /dev_stage="embryonic"
                     /lab_host="E.coli Electromax DH10B"
                     /clone_lib="squirrel embryo library 1"
                     /note="Vector: pFLC; Site_1: SalI GTCGAG; Site_2: BamHI
                     GGATCC; Normalized and subtracted cDNA library prepared
                     from embryos"
ORIGIN

  Query Match             52.8%;  Score 394.4;  DB 7;  Length 807;
  Best Local Similarity   73.5%;  Pred. No. 2.3e-101;
  Matches  548;  Conservative    0;  Mismatches  186;  Indels   12;  Gaps    3;

Qy          1 ATGTCCCTGTTTCCATCACTCCCTCTCCTTCTCCTGAGTATGGTGGCAGCGTCTTACTCA 60
              |||| |||||||||| ||||||| || |||||||||| ||||| ||| | |   ||||
Db         64 ATGTTCCTGTTTCCATTACTCCCTGTCTTTCTCCTGAGTGTGGTGACAGTGGC---CTCA 120

Qy         61 GAAACTGTGACCTGTGAGGATGCCCAAAAGACCTGCCCTGCAGTGATTGCCTGTAGCTCT 120
              |||||    || |||||||||||||| ||||||||  ||    |||||| ||||| |
Db        121 GAAACAAAAACATGTGAGGATGCCCAGAAGACCTGCTCT---GTGATTACCTGTGGGATC 177

Qy        121 CCAGGCATCAACGGCTTCCCAGGCAAAGATGGGCGTGATGGCACCAAGGGAGAAAAGGGG 180
              || | || |||||||   ||||||| ||||||||| |||||   ||||||||||||||||
Db        178 CCTGTCACCAACGGCACTCCAGGCAGAGATGGGCGAGATGGACTCAAGGGAGAAAAGGGA 237

Qy        181 GAACCAGGCCAAGGGCTCAGAGGCTTACAGGGCCCCCCTGGAAAGTTGGGGCCTCCAGGA 240
              || ||||| |||||||||||||| || |||||||| || || ||  ||||||||||||||
Db        238 GAGCCAGGTCAAGGGCTCAGAGGTTTGCAGGGCCCTCCAGGGAAACTGGGGCCTCCAGGA 297

Qy        241 AATCCAGGGCCTTCTGGGTCACCAGGACCAAAGGGCCAAAAAGGAGACCCTGGAAAAAGT 300
              ||| ||||| |  |||||| |||||||||| |||||||||||||| | |||| | |||
Db        298 AATACAGGGGCGCCTGGGGCTCCAGGACCAAGAGGCCAAAAAGGAGATCGTGGAGATAGT 357

Qy        301 CCGGATGGTGATAGTAGCCTGGCTGCCTCAGAAAG------AAAAGCTCTGCAAACAGAA 354
              ||| || ||| | ||  ||||||  || ||| ||      ||     ||| || |||||
Db        358 TCGGCTGCTGAGACTAAACTGGCTAACTTAGAGAGAGAGATAAGGAACCTGAAATCAGAA 417
```

```
Qy       355 ATGGCACGTATCAAAAAGTGGCTGACCTTCTCTCTGGGCAAACAAGTTGGGAACAAGTTC 414
Db       418 TTGGACCGCATTAAAAAGTTGCAAGCCTTCTCTTTGGGCAAAAAGTCTGGAAAGAAGTTC 477

Qy       415 TTCCTGACCAATGGTGAAATAATGACCTTTGAAAAAGTGAAGGCCTTGTGTGTCAAGTTC 474
Db       478 TACGTGACCAATGGTGAAAATATGCCTTTTTCCAAAGCGAAGGCTTGGTGCACAGAGCTC 537

Qy       475 CAGGCCTCTGTGGCCACCCCCAGGAATGCTGCAGAGAATGGAGCCATTCAGAATCTCATC 534
Db       538 CAGGCCACTGTGGCTGCCCCCAAGAATGCTGAGGAGAACAAGAACATCCAACAGGTGGCC 597

Qy       535 AAGGAGGAAGCCTTCCTGGGCATCACTGATGAGAAGACAGAAGGGCAGTTTGTGGATCTG 594
Db       598 AGAGACAATGTCTTCCTGGGTATCACAGATGAGGTTACAGAAGGCCAGTTTATGTATGTG 657

Qy       595 ACAGGAAATAGACTGACCTACACAAACTGGAACGAGGGTGAACCCAACAATGCTGGTTCT 654
Db       658 ACAGGAGGGAGGCTAACCTACAGCAACTGGAAGGCGAATGAGCCTAATAACCATGGCTCA 717

Qy       655 GATGAAGATTGTGTATTGCTACTGAAAAATGGCCAGTGGAATGACGTCCCCTGCTCCACC 714
Db       718 GGGGAGGACTGTGTGATTCTCTTGAAGGATGGACTCTGGAATGATGTTTCCTGCTCGTCC 777

Qy       715 TCCCATCTGGCCGTCTGTGAGTTCCC 740
Db       778 TCCTTCCCTGGTGTCTGTGAGTTCCC 803
```

RESULT 6
AY413288
LOCUS AY413288 735 bp DNA linear GSS 17-DEC-2003
DEFINITION Mus musculus MBL2 gene, VIRTUAL TRANSCRIPT, partial sequence, genomic survey sequence.
ACCESSION AY413288
VERSION AY413288.1 GI:39769250
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 735)
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.
TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous gene trios
JOURNAL Science 302 (5652), 1960-1963 (2003)
PUBMED 14671302
REFERENCE 2 (bases 1 to 735)
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.
TITLE Direct Submission
JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA
COMMENT This sequence was made by sequencing genomic exons and ordering them based on alignment.
FEATURES Location/Qualifiers
source 1. .735
/organism="Mus musculus"
/mol_type="genomic DNA"
/db_xref="taxon:10090"
gene <1. .>735
/gene="MBL2"
/locus_tag="HCM4840"
ORIGIN

Query Match 47.1%; Score 352.2; DB 9; Length 735;
Best Local Similarity 66.3%; Pred. No. 2.7e-89;
Matches 479; Conservative 0; Mismatches 237; Indels 6; Gaps 2;

```
Qy        26 TCCTTCTCCTGAGTATGGTGGCAGCGTCTTACTCAGAAACTGTGACCTGTGAGGATGCCC 85
Db        20 TCCTTCTGCTGTGTGTGGTGACAGTGGTTTATGCAGAGACCTTAACC---GAAGGTGTTC 76

Qy        86 AAAAGACCTGCCCTGCAGTGATTGCCTGTAGCTCTCCAGGCATCAACGGCTTCCCAGGCA 145
Db        77 AAAATTCCTGCCCT---GTGGTTACCTGCAGTTCTCCAGGCCTGAATGGCTTCCCAGGCA 133

Qy       146 AAGATGGGCGTGATGGCACCAAGGGAGAAAAGGGGGAACCAGGCCAAGGGCTCAGAGGCT 205
Db       134 AAGATGGACGTGACGGTGCCAAGGGAGAAAAGGGAGAACCAGGTCAAGGGCTCAGAGGCT 193

Qy       206 TACAGGGCCCCCCTGGAAAGTTGGGGCCTCCAGGAAATCCAGGGCCTTCTGGGTCACCAG 265
Db       194 TGCAAGGCCCTCCTGGAAAAGTAGGACCTACAGGACCCCCAGGGAATCCGGGGTTAAAAG 253

Qy       266 GACCAAAGGGCCAAAAAGGAGACCCTGGAAAAAGTCCGGATGGTGATAGTAGCCTGGCTG 325
Db       254 GAGCAGTGGGACCGAAAGGAGACCGTGGGGACAGAGCAGNNNNNNNNNNNNNNNNNNNN 313

Qy       326 CCTCAGAAAGAAAAGCTCTGCAAACAGAAATGGCACGTATCAAAAAGTGGCTGACCTTCT 385
Db       314 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNGGGTGCTCTTCT 373

Qy       386 CTCTGGGCAAACAAGTTGGGAACAAGTTCTTCCTGACCAATGGTGAAATAATGACCTTTG 445
Db       374 CTCTGAGTGAAAAAGTTGGAAAGAAGTATTTTGTGAGCAGTGTTAAAAAGATGAGCCTTG 433

Qy       446 AAAAAGTGAAGGCCTTGTGTGTCAAGTTCCAGGCCTCTGTGGCCACCCCCAGGAATGCTG 505
Db       434 ACAGAGTGAAGGCCCTGTGCTCCGAATTCCAGGGCTCTGTGGCCACTCCCAGGAATGCTG 493

Qy       506 CAGAGAATGGAGCCATTCAGAATCTCATCAAGGAGGAAGCCTTCCTGGGCATCACTGATG 565
Db       494 AGGAAAACTCGGCCATCCAGAAAGTGGCCAAAGATATTGCCTACTTGGGCATCACAGATG 553

Qy       566 AGAAGACAGAAGGGCAGTTTGTGGATCTGACAGGAAATAGACTGACCTACACAAACTGGA 625
Db       554 TGAGGGTTGAAGGCAGTTTTGAGGATCTGACAGGAAACAGAGTGCGCTATACTAATTGGA 613

Qy       626 ACGAGGGTGAACCCAACAATGCTGGTTCTGATGAAGATTGTGTATTGCTACTGAAAAATG 685
Db       614 ATGATGGGGAGCCCAACAACACGGGCGATGGGGAAGACTGTGTGGTGATCTTGGGAAATG 673

Qy       686 GCCAGTGGAATGACGTCCCCTGCTCCACCTCCCATCTGGCCGTCTGTGAGTTCCCTATCT 745
Db       674 GCAAGTGGAACGATGTCCCCTGCTCTGACTCTTTTTTGGCAATCTGTGAATTCTCTGACT 733

Qy       746 GA 747
Db       734 GA 735
```

RESULT 7
CO583176
LOCUS CO583176 977 bp mRNA linear EST 20-JUL-2004
DEFINITION ILLUMIGEN_MCQ_44503 Katze_MMLV Macaca mulatta cDNA clone IBIUW:18690 5' similar to Bases 266 to 879 highly similar to human Unigene Hs.102310, mRNA sequence.
ACCESSION CO583176
VERSION CO583176.1 GI:50415779
KEYWORDS EST.
SOURCE Macaca mulatta (rhesus monkey)
ORGANISM Macaca mulatta
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae; Cercopithecinae; Macaca.
REFERENCE 1 (bases 1 to 977)
AUTHORS Katze,M.G., Thomas,M., Korth,M., Iadonato,S.P. and Magness,C.L.
TITLE Large-scale Rhesus Macaque cDNA Sequencing
JOURNAL Unpublished (2003)
COMMENT Contact: C. Magness

Illumigen Biosciences Inc.
2203 Airport Way S, Suite 450, Seattle, WA 98134, USA
Tel: 2063780400
Fax: 2063780408
Email: cmagness@illumigen.com
Sequenced on 2004.06.17. 631 Q20 bases. Library Preparation: Prof. Michael Katze Lab at University of Washington DNA Sequencing: Illumigen Biosciences Inc. For further information, see http://www.macaque.org
PCR PRimers
FORWARD: CCCTCACTAAAGGGAACAAAA
BACKWARD: CACTATAGGGCGAATTGGGTA
Insert Length: 977 Std Error: 0.00
Plate: CL000398 row: C column: 06
Seq primer: CCCTCACTAAAGGGAACAAAA
POLYA=No.

```
FEATURES             Location/Qualifiers
     source          1. .977
                     /organism="Macaca mulatta"
                     /mol_type="mRNA"
                     /strain="Indian"
                     /db_xref="taxon:9544"
                     /clone="IBIUW:18690"
                     /sex="female"
                     /dev_stage="adult"
                     /lab_host="Electromax DH10B"
                     /clone_lib="Katze_MMLV"
                     /note="Organ: liver; Vector: pDONR 222; Site_1: BsrG I;
                     Site_2: BsrG I; Created from CloneMiner cDNA Library
                     Construction kit (catalog #18249-029)"
ORIGIN

  Query Match             45.3%;  Score 338.6;  DB 7;  Length 977;
  Best Local Similarity   72.5%;  Pred. No. 2.3e-85;
  Matches  469;  Conservative    0;  Mismatches  169;  Indels    9;  Gaps    2;

Qy          1 ATGTCCCTGTTTCCATCACTCCCTCTCCTTCTCCTGAGTATGGTGGCAGCGTCTTACTCA 60
              |||| ||||||||| ||| ||||| |||||||||||   | ||||| |||| || | |||
Db         85 ATGTTCCTGTTTCCGTCATTCCCTGTCCTTCTCCTGTCTGTGGTGACAGCTTCCTGCTCC 144

Qy         61 GAAACTGTGACCTGTGAGGATGCCCAAAAGACCTGCCCTGCAGTGATTGCCTGTAGCTCT 120
              |||||     |||||||||||||||| ||||||||| ||    |||||| ||||| ||
Db        145 GAAACAAAAGCCTGTGAGGATGCCCAGAAGACCTGCTCT---GTGATTACCTGTGGCATC 201

Qy        121 CCAGGCATCAACGGCTTCCCAGGCAAAGATGGGCGTGATGGCACCAAGGGAGAAAAGGGG 180
              || | || ||| |||  |||||||| ||||||||  |||||  |||||| ||||||||
Db        202 CCCGTCACCAATGGCACCCCAGGCAGAGATGGGCGAGATGGACCCAAGGGGGAAAAGGGA 261

Qy        181 GAACCAGGCCAAGGGCTCAGAGGCTTACAGGGCCCCCCTGGAAAGTTGGGGCCTCCAGGA 240
              || ||||| |||||||||||||| || |||||||| |||||  |||| |||||| |||||||
Db        262 GAGCCAGGTCAAGGGCTCAGAGGTTTGCAGGGCCCTCCTGGGAAGTCGGGGCCCCCAGGA 321

Qy        241 AATCCAGGGCCTTCTGGGTCACCAGGACCAAAGGGCCAAAAAGGAGACCCTGGAAAAAGT 300
              ||  ||||| || ||||    |||||||||| ||| |||||||||| | |||  | | |
Db        322 AACACAGGGGCTCCTGGAATTCCAGGACCAAGGGGACAAAAAGGAGATCATGGGGACAAT 381

Qy        301 CCGGATGGTGATAGTAGCCTGGCTGCCTCAGAAAGAAAAGCT------CTGCAAACAGAA 354
              | | || |||   ||  |||||   || ||| ||| |           |||  | |||||
Db        382 TCAGTTGCTGAGGCTAAGCTGGCCAACTTAGAGAGACAGCTACAGAGCCTGAGATCAGAA 441

Qy        355 ATGGCACGTATCAAAAAGTGGCTGACCTTCTCTCTGGGCAAACAAGTTGGGAACAAGTTC 414
              |||  |  || || |||  ||   |||||| |||| |||     |||||| ||| ||
Db        442 CTGGACCACATGAAGAAGCTGCAAGCCTTCTCCTTGGGGAAAATGTCTGGGAAGAAGCTC 501

Qy        415 TTCCTGACCAATGGTGAAATAATGACCTTTGAAAAAGTGAAGGCCTTGTGTGTCAAGTTC 474
              ||| ||||||| |||||    ||| | ||     |||||||||| ||||||    | ||
Db        502 TTCGTGACCAACGGTGAGCGGATGCCTTTCTCCGAAGTGAAGGCTCTGTGTGCTGGGCTC 561

Qy        475 CAGGCCTCTGTGGCCACCCCCAGGAATGCTGCAGAGAATGGAGCCATTCAGAATCTCATC 534
              |||||| | |||||  |||||| |||||| | ||||||    ||||| ||| || |   |
Db        562 CAGGCCACGGTGGCTGCCCCCAAGAATGCCGAGGAGAATAAGGCCATCCAGGATGTGGCC 621

Qy        535 AAGGAGGAAGCCTTCCTGGGCATCACTGATGAGAAGACAGAAGGGCAGTTTGTGGATCTG 594
```

```
              || ||    |||||||||||||||| ||||||   || ||||| |||||  || |  ||
Db        622 AAAGACACTGCCTTCCTGGGCATCACAGATGAGGCAACCGAAGGCCAGTTCATGTACGTG 681

Qy        595 ACAGGAAATAGACTGACCTACACAAACTGGAACGAGGGTGAACCCAA 641
              || ||    || |||||||||  ||||||||  ||| ||||||  ||
Db        682 ACGGGCGGAAGGCTGACCTACAGCAACTGGAAAAAGGATGAACCAAA 728


RESULT 8
BF537636
LOCUS       BF537636                828 bp    mRNA    linear   EST 11-DEC-2000
DEFINITION  602054516F1 NCI_CGAP_SG2 Mus musculus cDNA clone IMAGE:4193883 5',
            mRNA sequence.
ACCESSION   BF537636
VERSION     BF537636.1  GI:11625004
KEYWORDS    EST.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 828)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Jeffrey E. Green, M.D.
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM9526  row: o  column: 04
            High quality sequence stop: 757.
FEATURES             Location/Qualifiers
     source          1. .828
                     /organism="Mus musculus"
                     /mol_type="mRNA"
                     /strain="FVB/N"
                     /db_xref="taxon:10090"
                     /clone="IMAGE:4193883"
                     /lab_host="DH10B (T1 phage-resistant)"
                     /clone_lib="NCI_CGAP_SG2"
                     /note="Organ: salivary gland; Vector: pCMV-SPORT6; Site_1:
                     NotI; Site_2: SalI; Cloned unidirectionally. Primer: Oligo
                     dT. Average insert size 1.3 kb. Constructed by Life
                     Technologies. Note: this is a NCI_CGAP Library."
ORIGIN

  Query Match             44.8%;  Score 335;  DB 2;  Length 828;
  Best Local Similarity   71.5%;  Pred. No. 2.3e-84;
  Matches  511;  Conservative    0;  Mismatches  195;  Indels    9;  Gaps    5;

Qy         34 CTGAGTATGGTGGCAGCGTCTTACTCAGAAACTGTGACCTGTGAGGATGCCCAAAAGACC 93
              ||| || ||||| ||| |  |||  |||| ||  | |||   || | ||  |||||  ||
Db          3 CTGTGTGTGGTGACAGTGGTTTATGCAGAGACCTTAACC---GAAGGTGTTCAAAATTCC 59

Qy         94 TGCCCTGCAGTGATTGCCTGTAGCTCTCCAGGCATCAACGGCTTCCCAGGCAAAGATGGG 153
              ||||||    ||| || |||| || |||||||| | || ||||||||||||||||||||
Db         60 TGCCCT---GTGGTTACCTGCAGTTCTCCAGGCCTGAATGGCTTCCCAGGCAAAGATGGA 116

Qy        154 CGTGATGGCACCAAGGGAGAAAAGGGGGAACCAGGCCAAGGGCTCAGAGGCTTACAGGGC 213
              ||||| ||  |||||||||||||||| |||||||| |||||||||||||||| || |||
Db        117 CGTGACGGTGCCAAGGGAGAAAAGGGAGAACCAGGTCAAGGGCTCAGAGGCTTGCAAGGC 176

Qy        214 CCCCCTGGAAAGTTGGGGCCTCCAGGAAATCCAGGGCCTTCTGGGTCACCAGGACCAAAG 273
              || ||||||||   | ||  ||| |||||    ||||||   | | |||| |||| ||  |
Db        177 CCTCCTGGAAAAGTAGGACCTACAGGACCCCCAGGGAATCCGGGGTTAAAAGGAGCAGTG 236

Qy        274 GGCCAAAAAGGAGACCCTGGAAAAAGTCCGGATGGTGATAGTAGCCTGGCTGCCTCAGAA 333
              || | |||||||||| |||  | ||  | ||   |||||  |||||      ||  ||||||
Db        237 GGACCGAAAGGAGACCGTGGGGACAGAGCAGAATTTGATACTAGCGAAATTGATTCAGAA 296
```

```
Qy        334 AGAAAAGCTCTGCAAACAGAAATGGCACGTATCAAAAAGTGGCTGACCTTCTCTCTCTGGGC 393
              |    ||| || | | |||| ||  |   | | ||| ||| ||  ||||||||||  |
Db        297 ATTGCAGCCCTACGATCAGAGCTGAGAGCCCTGAGAAACTGGGTGCTCTTCTCTCTGAGT 356

Qy        394 AAACAAGTTGGGAACAAGTTCTTCCTGACCAATGGTGAAATAATGACCTTTGAAAAAGTG 453
              || ||||||| || ||| | ||  ||| || || | |||  |||| | |||| | ||||
Db        357 GAAAAAGTTGGAAAGAAG-TATTTGTGAGCAGTGTTAAAAAGATGAGCCTTGACAGAGTG 415

Qy        454 AAGGCCTTGTGTGTCAAGTTCCAGGCCTCTGTGGCCACCCCCAGGAATGCTGCAGAGAAT 513
              |||||| ||||   | | ||||||| |||||||||||| |||||||||||||  || ||
Db        416 AAGGCCCTGTGCTCCGAATTCCAGG-CTCTGTGGCCACTCCCAGGAATGCTGAGGAAAAC 474

Qy        514 GGAGCCATTCAGAATCTCATCAAGGAGGAAGCCTTCCTGGGCATCACTGATGAGAAGACA 573
              |||||  |||||  |   ||| ||    |||| | |||||||||| |||| || |
Db        475 TCGGCCATCCAGAAAGTGGCCAAAGATATTGCCTACTTGGGCATCACAGATGTGAGGGTT 534

Qy        574 GAAGGGCAGTTTGTGGATCTGACAGGAAATAGACTGACCTACACAAACTGGAACGAGGGT 633
              |||||    |||| |||||||||||||||| ||| ||  ||| || || ||||| || ||
Db        535 GAAGGCAGTTTTGAGGATCTGACAGGAAACAGAGTGCGCTATACTAATTGGAATGATGGG 594

Qy        634 GAACCCAACAATGCTGGTTCTGATGAAGATTGTGTATTGCTACTGAAAAATGGCCAGTGG 693
              || |||||||  | ||   ||  ||||| |||||  || |  ||  |||||||| |||||
Db        595 GAGCCCAACAACACGGGCGATGGGGAAGACTGTGTGGTGATCTTGGGAAATGGCAAGTGG 654

Qy        694 AATGACGTCCCCT-GCTCCACCTCCCATCTGGCCGTCTGTGAGTTCCCTATCTGA 747
              || ||  ||||||| ||||   |||   | ||||  ||||||| ||| ||  ||||
Db        655 AACGATGTCCCCTGGCTCTGACTCTTTTTTGGCAATCTGTGAATTCTCTGACTGA 709
```

RESULT 9
CK778513/c
LOCUS CK778513 722 bp mRNA linear EST 20-FEB-2004
DEFINITION 965675 MARC 3BOV Bos taurus cDNA 3', mRNA sequence.
ACCESSION CK778513
VERSION CK778513.1 GI:42730826
KEYWORDS EST.
SOURCE Bos taurus (cow)
ORGANISM Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovinae; Bos.
REFERENCE 1 (bases 1 to 722)
AUTHORS Smith,T.P.L., Grosse,W.M., Freking,B.A., Roberts,A.J., Stone,R.T., Casas,E., Wray,J.E., White,J., Cho,J., Fahrenkrug,S.C., Bennett,G.L., Heaton,M.P., Laegreid,W.W., Rohrer,G.A., Chitko-McKown,C.G., Pertea,G., Holt,I., Karamycheva,S., Liang,F., Quackenbush,J. and Keele,J.W.
TITLE Sequence evaluation of four pooled-tissue normalized bovine cDNA libraries and construction of a gene index for cattle
JOURNAL Genome Res. 11 (4), 626-630 (2001)
MEDLINE 21180013
PUBMED 11282978
COMMENT Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called with phred v0.020425.c and trimmed with the aid of the trim_alt option. Vector identified with cross_match v0.990329.
Plate: 66 row: E column: 1
Seq primer: GTAATACGACTCACTATAGGG.
FEATURES Location/Qualifiers
source 1. .722
/organism="Bos taurus"
/mol_type="mRNA"
/db_xref="taxon:9913"
/tissue_type="pooled"
/lab_host="DH10B"
/clone_lib="MARC 3BOV"
/note="Vector: pCMV SPORT6; Site_1: NotI; Site_2: SalI;

Library made from pooled tissue from marrow, alveolar macrophage, ovary, fetal semitendonosus muscle, and fetal longissimus muscle."
ORIGIN

Query Match 43.5%; Score 324.8; DB 7; Length 722;
Best Local Similarity 70.5%; Pred. No. 1.9e-81;
Matches 450; Conservative 0; Mismatches 182; Indels 6; Gaps 1;

```
Qy        116 GCTCTCCAGGCATCAACGGCTTCCCAGGCAAAGATGGGCGTGATGGCACCAAGGGAGAAA 175
              ||   || | || ||| |||  |||||||| |||||||| |||||  ||||||| ||||
Db        721 GCATCCCCGTCACCAATGGCACCCCAGGCAGAGATGGGCGAGATGGACCCAAGGGGGAAA 662

Qy        176 AGGGGGAACCAGGCCAAGGGCTCAGAGGCTTACAGGGCCCCCCTGGAAAGTTGGGGCCTC 235
              |||| || ||||| |||||||| ||||| || |||||||| ||||| |||| |||||| |
Db        661 AGGGAGAGCCAGGTCAAGGGCTTAGAGGTTTGCAGGGCCCTCCTGGGAAGTCGGGGCCCC 602

Qy        236 CAGGAAATCCAGGGCCTTCTGGGTCACCAGGACCAAAGGGCCAAAAAGGAGACCCTGGAA 295
              |||||||  ||||| || ||||    |||||||||| ||| |||||||||| | |||
Db        601 CAGGAAACACAGGGGCTCCTGGAATTCCAGGACCAAGGGGACAAAAAGGAGATCATGGGG 542

Qy        296 AAAGTCCGGATGGTGATAGTAGCCTGGCTGCCTCAGAAAG------AAAAGCTCTGCAAA 349
              | | | | || |||   ||  |||||   || ||| ||      | |   |||  |
Db        541 ACAATTCAGTTGCTGAGGCTAAGCTGGCCAACTTAGAGAGACAGCTACAGAGCCTGAGAT 482

Qy        350 CAGAAATGGCACGTATCAAAAAGTGGCTGACCTTCTCTCTGGGCAAACAAGTTGGGAACA 409
              |||||  |||  |  || || |||  ||   |||||||  |||| |||      |||||| |
Db        481 CAGAACTGGACCACATGAAGAAGCTGCAAGCCTTCTCCTTGGGGAAAATGTCTGGGAAGA 422

Qy        410 AGTTCTTCCTGACCAATGGTGAAATAATGACCTTTGAAAAAGTGAAGGCCTTGTGTGTCA 469
              || ||||| |||||||  |||||     |||  | ||      ||||||||||  ||||||
Db        421 AGCTCTTCGTGACCAACGGTGAGCAGATGCCTTTCTCCGAAGTGAAGGCTCTGTGTGCTG 362

Qy        470 AGTTCCAGGCCTCTGTGGCCACCCCCAGGAATGCTGCAGAGAATGGAGCCATTCAGAATC 529
              | |||||||| | |||||  ||||||  |||||| | |||||  |||||  ||| ||
Db        361 GGCTCCAGGCCACGGTGGCTGCCCCCAAGAATGCCGAGGAGAATAAGGCCATCCAGGATG 302

Qy        530 TCATCAAGGAGGAAGCCTTCCTGGGCATCACTGATGAGAAGACAGAAGGGCAGTTTGTGG 589
              |   ||| ||    |||||||||||||||||| ||||||   || |||||  |||||  ||
Db        301 TGGCCAAAGACACTGCCTTCCTGGGCATCACAGATGAGGCAACCGAAGGCCAGTTCATGT 242

Qy        590 ATCTGACAGGAAATAGACTGACCTACACAAACTGGAACGAGGGTGAACCCAACAATGCTG 649
              |  |||| ||    || |||||||||  ||||||||  ||| ||| || ||  |    |
Db        241 ACGTGACGGGCGGGAGGCTGACCTACAGCAACTGGAAGAAGGATGAGCCAAATGACCACG 182

Qy        650 GTTCTGATGAAGATTGTGTATTGCTACTGAAAAATGGCCAGTGGAATGACGTCCCCTGCT 709
              ||||  |  || || |||||  | || ||||  |||||  |  |||||||| || |||||
Db        181 GTTCAGGGGAGGACTGTGTGATTCTCCTGAGCAATGGGCTCTGGAATGACATCTCCTGCA 122

Qy        710 CCACCTCCCATCTGGCCGTCTGTGAGTTCCCTATCTGA 747
              |  |||||  |  | |||||||||||||| |||  ||||
Db        121 CGGCCTCCTACATCGCCGTCTGTGAGTTTCCTGCCTGA 84
```

RESULT 10
AV660023
LOCUS AV660023 367 bp mRNA linear EST 16-JAN-2002
DEFINITION AV660023 GLC Homo sapiens cDNA clone GLCGDC05 3', mRNA sequence.
ACCESSION AV660023
VERSION AV660023.1 GI:9881037
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 367)
AUTHORS Xu,X., Huang,J., Xu,Z., Qian,B., Zhu,Z., Yan,Q., Cai,T., Zhang,X., Xiao,H., Qu,J., Liu,F., Huang,Q., Cheng,Z., Li,N., Du,J., Hu,W., Shen,K., Lu,G., Fu,G., Zhong,M., Xu,S., Gu,W., Huang,W., Zhao,X., Hu,G., Gu,J., Chen,Z. and Han,Z.
TITLE Insight into hepatocellular carcinogenesis at transcriptome level by comparing gene expression profiles of hepatocellular carcinoma with those of corresponding noncancerous liver

```
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 98 (26), 15089-15094 (2001)
  MEDLINE   21625106
   PUBMED   11752456
COMMENT     Contact: Zeguang Han
            Chinese National Human Genome Center at Shanghai
            351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
            201203, P. R. China
            Tel: 86-21-50801919(ex.45)
            Fax: 86-21-50801922
            Email: hanzg@chgc.sh.cn
            This clone is available at CHGC in Shanghai.
FEATURES             Location/Qualifiers
     source          1. .367
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="GLCGDC05"
                     /tissue_type="corresponding non cancerous liver tissue"
                     /dev_stage="Adult"
                     /lab_host="SOLR"
                     /clone_lib="GLC"
                     /note="Vector: pBluescript sk(-); Site_1: EcoRI; Site_2:
                     XhoI"
ORIGIN

  Query Match             40.6%;  Score 303;  DB 1;  Length 367;
  Best Local Similarity   87.2%;  Pred. No. 2.6e-75;
  Matches  367;  Conservative    0;  Mismatches    0;  Indels   54;  Gaps    1;

Qy        174 AAAGGGGGAACCAGGCCAAGGGCTCAGAGGCTTACAGGGCCCCCCTGGAAAGTTGGGGCC 233
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 AAAGGGGGAACCAGGCCAAGGGCTCAGAGGCTTACAGGGCCCCCCTGGAAAGTTGGGGCC 60

Qy        234 TCCAGGAAATCCAGGGCCTTCTGGGTCACCAGGACCAAAGGGCCAAAAAGGAGACCCTGG 293
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TCCAGGAAATCCAGGGCCTTCTGGGTCACCAGGACCAAAGGGCCAAAAAGGAGACCCTGG 120

Qy        294 AAAAAGTCCGGATGGTGATAGTAGCCTGGCTGCCTCAGAAAGAAAAGCTCTGCAAACAGA 353
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 AAAAAGTCCGGATGGTGATAGTAGCCTGGCTGCCTCAGAAAGAAAAGCTCTGCAAACAGA 180

Qy        354 AATGGCACGTATCAAAAAGTGGCTGACCTTCTCTCTGGGCAAACAAGTTGGGAACAAGTT 413
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 AATGGCACGTATCAAAAAGTGGCTGACCTTCTCTCTGGGCAAACAAGTTGGGAACAAGTT 240

Qy        414 CTTCCTGACCAATGGTGAAATAATGACCTTTGAAAAAGTGAAGGCCTTGTGTGTCAAGTT 473
              |||||||||||||||||||||||||||||||
Db        241 CTTCCTGACCAATGGTGAAATAATGACCTTTG-------------------------- 272

Qy        474 CCAGGCCTCTGTGGCCACCCCCAGGAATGCTGCAGAGAATGGAGCCATTCAGAATCTCAT 533
                                          ||||||||||||||||||||||||||||||||||
Db        273 --------------------------ATGCTGCAGAGAATGGAGCCATTCAGAATCTCAT 306

Qy        534 CAAGGAGGAAGCCTTCCTGGGCATCACTGATGAGAAGACAGAAGGGCAGTTTGTGGATCT 593
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        307 CAAGGAGGAAGCCTTCCTGGGCATCACTGATGAGAAGACAGAAGGGCAGTTTGTGGATCT 366

Qy        594 G 594
              |
Db        367 G 367


RESULT 11
AI255533
LOCUS       AI255533                 657 bp    mRNA    linear   EST 12-NOV-1998
DEFINITION  ui55f12.y1 Sugano mouse liver mlia Mus musculus cDNA clone
            IMAGE:1886351 5' similar to gb:D11440 Mouse mRNA for P28a subunit
            of Ra-reactive factor, complete (MOUSE);, mRNA sequence.
ACCESSION   AI255533
VERSION     AI255533.1  GI:3863058
KEYWORDS    EST.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 657)
  AUTHORS   Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
            Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
            Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
            Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
            Waterston,R.
  TITLE     The WashU-HHMI Mouse EST Project
  JOURNAL   Unpublished (1996)
COMMENT     Contact: Marra M/Mouse EST Project
            WashU-HHMI Mouse EST Project
            Washington University School of MedicineP
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: mouseest@watson.wustl.edu
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            MGI:970675
            Seq primer: custom primer used
            High quality sequence stop: 488.
FEATURES             Location/Qualifiers
     source          1. .657
                     /organism="Mus musculus"
                     /mol_type="mRNA"
                     /strain="C57BL"
                     /db_xref="taxon:10090"
                     /clone="IMAGE:1886351"
                     /sex="female"
                     /dev_stage="adult"
                     /lab_host="DH10B"
                     /clone_lib="Sugano mouse liver mlia"
                     /note="Organ: liver; Vector: pME18S-FL3; Site_1: DraIII
                     (CACTGTGTG); Site_2: DraIII (CACCATGTG); 1st strand cDNA
                     was primed with an oligo(dT) primer
                     [ATGTGGCCTTTTTTTTTTTTTTTT]; double-stranded cDNA was
                     ligated to a  DraIII adaptor [TGTTGGCCTACTGG], digested
                     and cloned into distinct DraIII sites of the pME18S-FL3
                     vector (5' site CACTGTGTG, 3' site CACCATGTG). XhoI should
                     be used to isolate the cDNA insert.  Size selection was
                     performed to exclude fragments <1.5kb.  Library
                     constructed by Dr. Sumio Sugano (University of Tokyo
                     Institute of Medical Science).  Custom primers  for
                     sequencing: 5' end primer CTTCTGCTCTAAAAGCTGCG and 3' end
                     primer CGACCTGCAGCTCGAGCACA."
ORIGIN

  Query Match             40.5%;  Score 302.2;  DB 1;  Length 657;
  Best Local Similarity   71.5%;  Pred. No. 5.4e-75;
  Matches  397;  Conservative    0;  Mismatches  158;  Indels    0;  Gaps    0;

Qy        101 CAGTGATTGCCTGTAGCTCTCCAGGCATCAACGGCTTCCCAGGCAAAGATGGGCGTGATG 160
              | ||| || |||| || ||||||||| | || ||||||||||||||||||||| ||||| |
Db         19 CTGTGGTTACCTGCAGTTCTCCAGGCCTGAATGGCTTCCCAGGCAAAGATGGACGTGACG 78

Qy        161 GCACCAAGGGAGAAAAGGGGGAACCAGGCCAAGGGCTCAGAGGCTTACAGGGCCCCCCTG 220
              |  |||||||||||||||| |||||||| |||||||||||||||| || ||||| ||||
Db         79 GTGCCAAGGGAGAAAAGGGAGAACCAGGTCAAGGGCTCAGAGGCTTGCAAGGCCCTCCTG 138

Qy        221 GAAAGTTGGGGCCTCCAGGAAATCCAGGGCCTTCTGGGTCACCAGGACCAAAGGGCCAAA 280
              ||||  | || ||| |||||   ||||||  | | |||| |  |||| ||  ||| |  |
Db        139 GAAAAGTAGGACCTACAGGACCCCCAGGGAATCCGGGGTTAAAAGGAGCAGTGGGACCGA 198

Qy        281 AAGGAGACCCTGGAAAAAGTCCGGATGGTGATAGTAGCCTGGCTGCCTCAGAAAGAAAAG 340
              |||||||||| |||  | ||  | ||   ||||| ||||      ||  |||||||    ||
Db        199 AAGGAGACCGTGGGGACAGAGCAGAATTTGATACTAGCGAAATTGATTCAGAAATTGCAG 258

Qy        341 CTCTGCAAACAGAAATGGCACGTATCAAAAAGTGGCTGACCTTCTCTCTCTGGGCAAACAAG 400
              | || | | ||||  ||  |    | | ||| ||| ||  ||||||||| |  || |||
Db        259 CCCTACGATCAGAGCTGAGAGCCCTGAGAAACTGGGTGCTCTTCTCTCTGAGTGAAAAAG 318

Qy        401 TTGGGAACAAGTTCTTCCTGACCAATGGTGAAATAATGACCTTTGAAAAAGTGAAGGCCT 460
```

```
Db        319 TTGGAAAGAAGTATTTTGTGAGCAGTGTTAAAAAGATGAGCCTTGACAGAGTGAAGGCCC 378

Qy        461 TGTGTGTCAAGTTCCAGGCCTCTGTGGCCACCCCCAGGAATGCTGCAGAGAATGGAGCCA 520

Db        379 TGTGCTCCGAATTCCAGGGCTCTGTGGCCACTCCCAGGAATGCTGAGGAAAACTCGGCCA 438

Qy        521 TTCAGAATCTCATCAAGGAGGAAGCCTTCCTGGGCATCACTGATGAGAAGACAGAAGGGC 580

Db        439 TCCAGAAAGTGGCCAAAGATATTGCCTACTTGGGCATCACAGATGTGAGGGTTGAAGGCA 498

Qy        581 AGTTTGTGGATCTGACAGGAAATAGACTGACCTACACAAACTGGAACGAGGGTGAACCCA 640

Db        499 GCTTTGAGGATCTGACAGGAAACAGAGTGCGCTATTCTAATTGGAATGGATGGGAACCCC 558

Qy        641 ACAATGCTGGTTCTG 655

Db        559 ACACCACGGGCGATG 573
```

RESULT 12
AY325174
LOCUS AY325174 1162 bp mRNA linear HTC 26-JUL-2003
DEFINITION Rattus norvegicus Ab2-011 mRNA, complete cds.
ACCESSION AY325174
VERSION AY325174.1 GI:33086525
KEYWORDS HTC.
SOURCE Rattus norvegicus (Norway rat)
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
REFERENCE 1 (bases 1 to 1162)
AUTHORS Xu,C.S., Li,W.Q., Li,Y.C., Han,H.P., Wang,G.P., Chai,L.Q., Yuan,J.Y., Yang,K.J., Yan,H.M., Chang,C.F., Zhao,L.F., Ma,H., Wang,L., Wang,S.F., Shi,J.B., Rahman,S., Wang,Q.N. and Zhang,J.B.
TITLE Liver regeneration after PH
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1162)
AUTHORS Xu,C.S., Li,W.Q., Li,Y.C., Han,H.P., Wang,G.P., Chai,L.Q., Yuan,J.Y., Yang,K.J., Yan,H.M., Chang,C.F., Zhao,L.F., Ma,H., Wang,L., Wang,S.F., Shi,J.B., Rahman,S., Wang,Q.N. and Zhang,J.B.
TITLE Direct Submission
JOURNAL Submitted (16-JUN-2003) Henan Bioengineering Key Lab, Henan Normal University, NO. 148 Jianshe Road, Xinxiang City, Henan 453002, P.R. China
FEATURES Location/Qualifiers
source 1. .1162
/organism="Rattus norvegicus"
/mol_type="mRNA"
/db_xref="taxon:10116"
CDS 41. .1156
/note="liver regeneration-related protein LRRG037"
/codon_start=1
/product="Ab2-011"
/protein_id="AAP92575.1"
/db_xref="GI:33086526"
/translation="MSLFTSFLLLCVLTAVYAETLTEGAQSSCPVIACSSPGLNGFPG
KDGHDGAKGEKGEPGQGLRGLQGPPGKVGPAGPPGNPGSKGATGPKGDRGESVEFDTT
NIDLEIAALRSELRAMRKWVLLSMSENVGKKYFMSSVRRMPLNRAKALCSELQGTVAT
PRNAEENRAIQNVAKDVAFLGITDQRTENVFEDLTGNRVRYTNWNEGRLSLRGPELHG
PAANSVYYTPSSSDTENIPPTEETAKDGCALDPYEQSLIHAATESKANSENQHYTLEK
QSVHISVVSVEFLVNLQMFAVTVSSHITRGNRRSLTPGLTHEDFPHKQADSPSLELTG
WLDRMASEPAGCSGLPSCSTRIVDVCQVYLDTMTMFV"
ORIGIN

Query Match 40.3%; Score 301.4; DB 3; Length 1162;
Best Local Similarity 70.6%; Pred. No. 1.1e-74;
Matches 401; Conservative 0; Mismatches 167; Indels 0; Gaps 0;

```
Qy         65 CTGTGACCTGTGAGGATGCCCAAAAGACCTGCCCTGCAGTGATTGCCTGTAGCTCTCCAG 124

Db         93 CCGAGACCTTAACCGAAGGGGCTCAAAGTAGCTGCCCTGTGATTGCCTGCAGTTCTCCGG 152

Qy        125 GCATCAACGGCTTCCCAGGCAAAGATGGGCGTGATGGCACCAAGGGAGAAAAGGGGGAAC 184

Db        153 GCCTGAACGGCTTCCCAGGCAAAGATGGACACGACGGTGCCAAGGGAGAAAAGGGAGAAC 212

Qy        185 CAGGCCAAGGGCTCAGAGGCTTACAGGGCCCCCCTGGAAAGTTGGGGCCTCCAGGAAATC 244

Db        213 CGGGTCAAGGCCTCAGAGGCTTGCAGGGCCCTCCTGGAAAAGTAGGACCTGCAGGGCCCC 272

Qy        245 CAGGGCCTTCTGGGTCACCAGGACCAAAGGGCCAAAAAGGAGACCCTGGAAAAAGTCCGG 304

Db        273 CAGGGAATCCTGGGTCAAAAGGAGCAACGGGACCAAAAGGAGACCGTGGAGAGAGTGTAG 332

Qy        305 ATGGTGATAGTAGCCTGGCTGCCTCAGAAAGAAAAGCTCTGCAAACAGAAATGGCACGTA 364

Db        333 AATTTGATACTACCAACATTGATTTAGAAATTGCAGCCCTGCGATCGGAGCTGAGAGCTA 392

Qy        365 TCAAAAAGTGGCTGACCTTCTCTCTGGGCAAACAAGTTGGGAACAAGTTCTTCCTGACCA 424

Db        393 TGAGAAAGTGGGTGCTCCTTTCTATGAGTGAAAATGTTGGAAAGAAGTACTTCATGAGCA 452

Qy        425 ATGGTGAAATAATGACCTTTGAAAAAGTGAAGGCCTTGTGTGTCAAGTTCCAGGCCTCTG 484

Db        453 GTGTTAGAAGGATGCCCCTTAACAGAGCGAAGGCTCTGTGCTCCGAACTCCAGGGCACTG 512

Qy        485 TGGCCACCCCCAGGAATGCTGCAGAGAATGGAGCCATTCAGAATCTCATCAAGGAGGAAG 544

Db        513 TGGCCACTCCCAGGAATGCTGAGGAAAATAGGGCCATCCAGAATGTGGCCAAAGATGTTG 572

Qy        545 CCTTCCTGGGCATCACTGATGAGAAGACAGAAGGGCAGTTTGTGGATCTGACAGGAAATA 604

Db        573 CCTTCTTGGGCATAACGGACCAGAGGACTGAAAACGTTTTTGAGGACCTGACAGGAAACA 632

Qy        605 GACTGACCTACACAAACTGGAACGAGGG 632

Db        633 GAGTGCGCTACACTAACTGGAATGAGGG 660
```

RESULT 13
AY325178
LOCUS AY325178 1162 bp mRNA linear HTC 26-JUL-2003
DEFINITION Rattus norvegicus Ab2-001 mRNA, complete cds.
ACCESSION AY325178
VERSION AY325178.1 GI:33086533
KEYWORDS HTC.
SOURCE Rattus norvegicus (Norway rat)
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
REFERENCE 1 (bases 1 to 1162)
AUTHORS Xu,C.S., Li,W.Q., Li,Y.C., Ma,H., Wang,L., Wang,S.F., Han,H.P., Wang,G.P., Chai,L.Q., Yuan,J.Y., Yang,K.J., Yan,H.M., Chang,C.F., Zhao,L.F., Shi,J.B., Rahman,S., Wang,Q.N. and Zhang,J.B.
TITLE Liver regeneration after PH
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1162)
AUTHORS Xu,C.S., Li,W.Q., Li,Y.C., Ma,H., Wang,L., Wang,S.F., Han,H.P., Wang,G.P., Chai,L.Q., Yuan,J.Y., Yang,K.J., Yan,H.M., Chang,C.F., Zhao,L.F., Shi;J.B., Rahman,S., Wang,Q.N. and Zhang,J.B.
TITLE Direct Submission
JOURNAL Submitted (16-JUN-2003) Henan Bioengineering Key Lab, Henan Normal University, NO. 148 Jianshe Road, Xinxiang City, Henan 453002, P.R. China
FEATURES Location/Qualifiers
source 1. .1162
/organism="Rattus norvegicus"
/mol_type="mRNA"
/db_xref="taxon:10116"
CDS 41. .1156
/note="liver regeneration-related protein LRRG053"
/codon_start=1
/product="Ab2-001"

/protein_id="AAP92579.1"
/db_xref="GI:33086534"
/translation="MSLFTSFLLLCVLTAVYAETLTEGAQSSCPVIACSSPGLNGFPG
KDGHDGAKGEKGEPGQGLRGLQGPPGKVGPAGPPGNPGSKGATGPKGDRGESVEFDTT
NIDLEIAALRSELRAMRKWVLLSMSENVGKKYFMSSVRRMPLNRAKALCSELQGTVAT
PRNAEENRAIQNVAKDVAFLGITDQRTENVFEDLTGNRVRYTNWNEGRLSLRGPELHG
PAANSVYYTPSSSDTENIPPTEETAKDGCALDPYEQSLIHAATESKANSENQHYTLEK
QSVHISVVSVEFLVNLQMFAVTVSSHITRGNRRSLTPGLTHEDFPHKQADSPSLELTG
WLDRMASEPAGCSGLPSCSTRIVDVCQVYLDTMTMFV"

ORIGIN

Query Match 40.3%; Score 301.4; DB 3; Length 1162;
Best Local Similarity 70.6%; Pred. No. 1.1e-74;
Matches 401; Conservative 0; Mismatches 167; Indels 0; Gaps 0;

```
Qy      65 CTGTGACCTGTGAGGATGCCCAAAAGACCTGCCCTGCAGTGATTGCCTGTAGCTCTCCAG 124
           | | |||||     || |      | |   ||    | ||||||||||| || ||||| |
Db      93 CCGAGACCTTAACCGAAGGGGCTCAAAGTAGCTGCCCTGTGATTGCCTGCAGTTCTCCGG 152

Qy     125 GCATCAACGGCTTCCCAGGCAAAGATGGGCGTGATGGCACCAAGGGAGAAAAGGGGGAAC 184
           || | |||||||||||||||||||||| |  || ||  ||||||||||||||||| ||||
Db     153 GCCTGAACGGCTTCCCAGGCAAAGATGGACACGACGGTGCCAAGGGAGAAAAGGGAGAAC 212

Qy     185 CAGGCCAAGGGCTCAGAGGCTTACAGGGCCCCCCTGGAAAGTTGGGGCCTCCAGGAAATC 244
           | || ||||| |||||||||| |||||||| ||||||||  | || ||| ||||    |
Db     213 CGGGTCAAGGCCTCAGAGGCTTGCAGGGCCCTCCTGGAAAAGTAGGACCTGCAGGGCCCC 272

Qy     245 CAGGGCCTTCTGGGTCACCAGGACCAAAGGGCCAAAAAGGAGACCCTGGAAAAAGTCCGG 304
           |||||  | ||||||||  |||| ||| ||| | ||||||||||| |||| | |||   |
Db     273 CAGGGAATCCTGGGTCAAAAGGAGCAACGGGACCAAAAGGAGACCGTGGAGAGAGTGTAG 332

Qy     305 ATGGTGATAGTAGCCTGGCTGCCTCAGAAAGAAAAGCTCTGCAAACAGAAATGGCACGTA 364
           |  ||||| || |     ||  | |||||    ||| |||| | | ||  ||  |  ||
Db     333 AATTTGATACTACCAACATTGATTTAGAAATTGCAGCCCTGCGATCGGAGCTGAGAGCTA 392

Qy     365 TCAAAAAGTGGCTGACCTTCTCTCTGGGCAAACAAGTTGGGAACAAGTTCTTCCTGACCA 424
           | | ||||||| ||  | | ||| || |  || | ||||| || |||| |||| ||| ||
Db     393 TGAGAAAGTGGGTGCTCCTTTCTATGAGTGAAAATGTTGGAAAGAAGTACTTCATGAGCA 452

Qy     425 ATGGTGAAATAATGACCTTTGAAAAAGTGAAGGCCTTGTGTGTCAAGTTCCAGGCCTCTG 484
           || |  ||  ||| || || | | || ||||||  ||||   | |  |||||| | |||
Db     453 GTGTTAGAAGGATGCCCCTTAACAGAGCGAAGGCTCTGTGCTCCGAACTCCAGGGCACTG 512

Qy     485 TGGCCACCCCCAGGAATGCTGCAGAGAATGGAGCCATTCAGAATCTCATCAAGGAGGAAG 544
           ||||||| |||||||||||||  || ||| | ||||| ||||||  |   ||| || |  |
Db     513 TGGCCACTCCCAGGAATGCTGAGGAAAATAGGGCCATCCAGAATGTGGCCAAAGATGTTG 572

Qy     545 CCTTCCTGGGCATCACTGATGAGAAGACAGAAGGGCAGTTTGTGGATCTGACAGGAAATA 604
           |||||  |||||||  || ||  ||| ||| |||      |||| ||| ||||||||||| |
Db     573 CCTTCTTGGGCATAACGGACCAGAGGACTGAAAACGTTTTTGAGGACCTGACAGGAAACA 632

Qy     605 GACTGACCTACACAAACTGGAACGAGGG 632
           || ||  |||||| |||||||| |||||
Db     633 GAGTGCGCTACACTAACTGGAATGAGGG 660
```

RESULT 14
AI195233/c

```
LOCUS       AI195233                 869 bp    mRNA    linear   EST 14-OCT-1998
DEFINITION  ui62c03.x1 Sugano mouse liver mlia Mus musculus cDNA clone
            IMAGE:1886980 3' similar to gb:X15422_cds1 MANNOSE-BINDING PROTEIN
            C PRECURSOR (HUMAN); gb:D11440 Mouse mRNA for P28a subunit of
            Ra-reactive factor, complete (MOUSE);, mRNA sequence.
ACCESSION   AI195233
VERSION     AI195233.1  GI:3747839
KEYWORDS    EST.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 869)
  AUTHORS   Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
            Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
            Schellenberg,K., Steptoe,M., Tan,P., Underwood,K., Moore,B.,
            Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
            Waterston,R.
  TITLE     The WashU-HHMI Mouse EST Project
  JOURNAL   Unpublished (1996)
COMMENT     Contact: Marra M/Mouse EST Project
            WashU-HHMI Mouse EST Project
            Washington University School of MedicineP
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: mouseest@watson.wustl.edu
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            MGI:971304
            Seq primer: custom primer used
            High quality sequence stop: 428.
FEATURES             Location/Qualifiers
     source          1. .869
                     /organism="Mus musculus"
                     /mol_type="mRNA"
                     /strain="C57BL"
                     /db_xref="taxon:10090"
                     /clone="IMAGE:1886980"
                     /sex="female"
                     /dev_stage="adult"
                     /lab_host="DH10B"
                     /clone_lib="Sugano mouse liver mlia"
                     /note="Organ: liver; Vector: pME18S-FL3; Site_1: DraIII
                     (CACTGTGTG); Site_2: DraIII (CACCATGTG); 1st strand cDNA
                     was primed with an oligo(dT) primer
                     [ATGTGGCCTTTTTTTTTTTTTTTT]; double-stranded cDNA was
                     ligated to a  DraIII adaptor [TGTTGGCCTACTGG], digested
                     and cloned into distinct DraIII sites of the pME18S-FL3
                     vector (5' site CACTGTGTG, 3' site CACCATGTG). XhoI should
                     be used to isolate the cDNA insert.  Size selection was
                     performed to exclude fragments <1.5kb.  Library
                     constructed by Dr. Sumio Sugano (University of Tokyo
                     Institute of Medical Science).  Custom primers  for
                     sequencing: 5' end primer CTTCTGCTCTAAAAGCTGCG and 3' end
                     primer CGACCTGCAGCTCGAGCACA."
```

ORIGIN

Query Match 39.1%; Score 292.4; DB 1; Length 869;
Best Local Similarity 67.0%; Pred. No. 3.8e-72;
Matches 424; Conservative 0; Mismatches 208; Indels 1; Gaps 1;

```
Qy     115 AGCTCTCCAGGCATCAACGGCTTCCCAGGCAAAGATGGGCGTGATGGCACCAAGGGAGAA 174
           || |||| |||| | || | || || ||  ||     || ||| | ||  | |||||||||
Db     805 AGTTCTCAAGGCCTGAATGCCTACCNAGCAAAGATGGGACGTNACGGTGCAAAGGGAGAA 746

Qy     175 AAGGGGGAACCAGGCCAAGGGCTCAGAGGCTTACAGGGCCCCCCTGGAAAGTTGGGGCCT 234
           ||||  ||| |||| ||||||||||||| |   |     | ||| |||  |||    || |
Db     745 AAGGAAGAAGCAGGTCAAGGGCTCAGATGGCTTGCAAGGCCCTCTGNNAAGAGTAGGACG 686

Qy     235 CCAGGAAATCCAGGGCCTTCTGGGTCACCAGGACCAAAGGGCCAAAAAGGAGACCCTGGA 294
           | |  |   ||   || |||| |  |||| ||   |   || ||||||||||| ||
Db     685 TACAGGACCCNCAGGGAATCGGGGTTAAAAGGAGCAGTGTACCGAAAAGGAGACCGTGNG 626

Qy     295 AAAAGTCCGGATGGTGATAGTAGCCTGGCTGCCTCAGAAAGAAAAGCTCTGCAAACAGAA 354
           | ||  | ||   ||||| ||||     ||  |||||||     ||| || | | ||||
Db     625 GACAGAGCAGAATTTGATACTAGCGAAATTGATTCAGAAATTGCAGCCCTACGATCAGAG 566

Qy     355 ATGGCACGTATCAAAAAGTGGCTGACCTTCTCTCTGGGCAAACAAGTTGGGAACAAGTTC 414
           ||  |    | | ||||||| ||  |||||||||| |  | ||| ||| || ||||
Db     565 CTGAGAGCCCTGAGAAAGTGGGTGCTCTTCTCTCTGAGTGANAAAG-TGGAAAGAAGTAT 507

Qy     415 TTCCTGACCAATGGTGAAATAATGACCTTTGAAAAAGTGAAGGCCTTGTGTGTCAAGTTC 474
           ||  ||| || || | |||  |||| | |||| | |||||||||| ||||   | | |||
Db     506 TTTGTGAGCAGTGTTAAAAAGATGAGCCTTGACAGAGTGAAGGCCCTGTGCTCCGAATTC 447

Qy     475 CAGGCCTCTGTGGCCACCCCCAGGAATGCTGCAGAGAATGGAGCCATTCAGAATCTCATC 534
           |||| |||||||||||| |||||||||||||  || ||   ||||| |||||  |   |
```

```
Db        446 CAGGGCTCTGTGGCCACTCCCAGGAATGCTGAGGAAAACTCGGCCATCCAGAAAGTGGCC 387

Qy        535 AAGGAGGAAGCCTTCCTGGGCATCACTGATGAGAAGACAGAAGGGCAGTTTGTGGATCTG 594
              || ||    |||| | |||||||||| |||| || |   |||||    |||| |||||||
Db        386 AAAGATATTGCCTACTTGGGCATCACAGATGTGAGGGTTGAAGGCAGTTTTGAGGATCTG 327

Qy        595 ACAGGAAATAGACTGACCTACACAAACTGGAACGAGGGTGAACCCAACAATGCTGGTTCT 654
              |||||||| ||| ||  ||| || || ||||| || || || ||||||||  | ||   |
Db        326 ACAGGAAACAGAGTGCGCTATACTAATTGGAATGATGGGGAGCCCAACAACACGGGCGAT 267

Qy        655 GATGAAGATTGTGTATTGCTACTGAAAAATGGCCAGTGGAATGACGTCCCCTGCTCCACC 714
              |  ||||| ||||| || |  ||  ||||||| ||||||| || ||||||||||   |
Db        266 GGGGAAGACTGTGTGGTGATCTTGGGAAATGGCAAGTGGAACGATGTCCCCTGCTCTGAC 207

Qy        715 TCCCATCTGGCCGTCTGTGAGTTCCCTATCTGA 747
              ||   | ||||  ||||||| ||| ||  ||||
Db        206 TCTTTTTTGGCAATCTGTGAATTCTCTGACTGA 174


RESULT 15
AV660367
LOCUS       AV660367                367 bp    mRNA    linear   EST 16-JAN-2002
DEFINITION  AV660367 GLC Homo sapiens cDNA clone GLCGGH07 3', mRNA sequence.
ACCESSION   AV660367
VERSION     AV660367.1  GI:9881381
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 367)
  AUTHORS   Xu,X., Huang,J., Xu,Z., Qian,B., Zhu,Z., Yan,Q., Cai,T., Zhang,X.,
            Xiao,H., Qu,J., Liu,F., Huang,Q., Cheng,Z., Li,N., Du,J., Hu,W.,
            Shen,K., Lu,G., Fu,G., Zhong,M., Xu,S., Gu,W., Huang,W., Zhao,X.,
            Hu,G., Gu,J., Chen,Z. and Han,Z.
  TITLE     Insight into hepatocellular carcinogenesis at transcriptome level
            by comparing gene expression profiles of hepatocellular carcinoma
            with those of corresponding noncancerous liver
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 98 (26), 15089-15094 (2001)
  MEDLINE   21625106
   PUBMED   11752456
COMMENT     Contact: Zeguang Han
            Chinese National Human Genome Center at Shanghai
            351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
            201203, P. R. China
            Tel: 86-21-50801919(ex.45)
            Fax: 86-21-50801922
            Email: hanzg@chgc.sh.cn
            This clone is available at CHGC in Shanghai.
FEATURES             Location/Qualifiers
     source          1. .367
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="GLCGGH07"
                     /tissue_type="corresponding non cancerous liver tissue"
                     /dev_stage="Adult"
                     /lab_host="SOLR"
                     /clone_lib="GLC"
                     /note="Vector: pBluescript sk(-); Site_1: EcoRI; Site_2:
                     XhoI"
ORIGIN

  Query Match             39.0%;  Score 291;  DB 1;  Length 367;
  Best Local Similarity   86.9%;  Pred. No. 7.2e-72;
  Matches  366;  Conservative    0;  Mismatches    0;  Indels   55;  Gaps    2;

Qy        174 AAAGGGGGAACCAGGCCAAGGGCTCAGAGGCTTACAGGGCCCCCCTGGAAAGTTGGGGCC 233
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 AAAGGGGGAACCAGGCCAAGGGCTCAGAGGCTTACAGGGCCCCCCTGGAAAGTTGGGGCC 60

Qy        234 TCCAGGAAATCCAGGGCCTTCTGGGTCACCAGGACCAAAGGGCCAAAAAGGAGACCCTGG 293
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

```
Db         61 TCCAGGAAATCCAGGGCCTTCTGGGTCACCAGGACCAAAGGGCCAAAAAGGAGACCCTGG 120

Qy        294 AAAAAGTCCGGATGGTGATAGTAGCCTGGCTGCCTCAGAAAGAAAAGCTCTGCAAACAGA 353
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 AAAAAGTCCGGATGGTGATAGTAGCCTGGCTGCCTCAGAAAGAAAAGCTCTGCAAACAGA 180

Qy        354 AATGGCACGTATCAAAAAGTGGCTGACCTTCTCTCTGGGCAAACAAGTTGGGAACAAGTT 413
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 AATGGCACGTATCAAAAAGTGGCTGACCTTCTCTCTGGGCAAACAAGTTGGGAACAAGTT 240

Qy        414 CTTCCTGACCAATGGTGAAATAATGACCTTTGAAAAAGTGAAGGCCTTGTGTGTCAAGTT 473
              ||||||||||||||||||||||||||||||||
Db        241 CTTCCTGACCAATGGTGAAATAATGACCTTTG---------------------------- 272

Qy        474 CCAGGCCTCTGTGGCCACCCCCAGGAATGCTGCAGAGAATGGAGCCATTCAGAATCTCAT 533
                                              ||||||||||||||||||||||||||||||
Db        273 ------------------------ATGCTGCAGAGAATGGAGCCATTCAGAATCTCAT 306

Qy        534 CAAGGAGGAAGCCTTCCTGGGCATCACTGATGAGAAGACAGAAGGGCAGTTTGTGGATCT 593
              |||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Db        307 CAAGGAGGAAGCCTTCCT-GGCATCACTGATGAGAAGACAGAAGGGCAGTTTGTGGATCT 365

Qy        594 G 594
              |
Db        366 G 366


Search completed: June 20, 2005, 18:00:16
Job time : 3230 secs
```

THIS PAGE BLANK (USPTO)